

Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala
 275 280 285

Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala
 290 295 300

Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp
 305 310 315 320

His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala
 325 330 335

Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp
 340 345 350

Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val
 355 360 365

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg
 370 375 380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly
 385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn
 405 410 415

Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val
 420 425 430

Leu Arg Gly Lys Val Thr Cys Ala Asp Gly Val Ala Gln Asn Ala
 435 440 445

<210> 979

<211> 1025

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1002)

<223> EXA02208

<400> 979

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 Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys
 1 5 10 15

atc atc gca gtg cac gat gat tcc ctc tcc cag gaa gtc ttc ggc gtc 96
 Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val
 20 25 30

acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca 144
 Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
 35 40 45

tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt 192
 Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
 50 55 60

ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt 240
 Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu
 65 70 75 80

ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac 288
 Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn
 85 90 95

aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc 336
 Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser
 100 105 110

acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct 384
 Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala
 115 120 125

gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat 432
 Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp
 130 135 140

ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt 480
 Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly
 145 150 155 160

ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca 528
 Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala
 165 170 175

gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac 576
 Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp
 180 185 190

ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc 624
 Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu
 195 200 205

aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc 672
 Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly
 210 215 220

ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc 720
 Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile
 225 230 235 240

tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc 768
 Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu
 245 250 255

tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc 816
 Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile
 260 265 270

agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt 864
 Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu
 275 280 285

ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga 912
 Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg
 290 295 300

gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc 960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac
 1002

Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn
 325 330

taaacagacc aaacacacgt gcc
 1025

<210> 980

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 980

Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys
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Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val
 20 25 30

Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

<400> 981																	
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taaacctcaa tcatcaaatt agggaagggc tgggaaatcc																	115
										atg	tca	tct	aat	tcc			
										Met	Ser	Ser	Asn	Ser			
										1				5			
att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta																	163
Ile	Asn	Ala	Glu	Ala	Arg	Ala	Glu	Leu	Ala	Glu	Leu	Ile	Lys	Glu	Leu		
				10					15					20			
gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat																	211
Ala	Val	Val	His	Gly	Glu	Val	Thr	Leu	Ser	Ser	Gly	Lys	Lys	Ala	Asp		
			25					30					35				
tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc																	259
Tyr	Tyr	Ile	Asp	Val	Arg	Arg	Ala	Thr	Leu	His	Ala	Arg	Ala	Ser	Arg		
		40					45					50					
ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac																	307
Leu	Ile	Gly	Gln	Leu	Leu	Arg	Glu	Ala	Thr	Ala	Asp	Trp	Asp	Tyr	Asp		
	55					60					65						
gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc																	355
Ala	Val	Gly	Gly	Leu	Thr	Leu	Gly	Ala	Asp	Pro	Val	Ala	Thr	Ala	Ile		
	70				75					80					85		
atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag																	403
Met	His	Ala	Asp	Gly	Arg	Asp	Ile	Asn	Ala	Phe	Val	Val	Arg	Lys	Glu		
				90					95					100			

gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451
 Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr
 105 110 115

 ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499
 Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser
 120 125 130

 cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547
 Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val
 135 140 145

 ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595
 Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile
 150 155 160 165

 gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643
 Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu
 170 175 180

 gga ctc aac taacaccccc ggccccacgg agt 675
 Gly Leu Asn

<210> 982

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 982

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 Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser
 20 25 30

 Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His
 35 40 45

 Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala
 50 55 60

 Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro
 65 70 75 80

 Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe
 85 90 95

 Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu
 100 105 110

 Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr
 115 120 125

 Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala
 130 135 140

 Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly
 145 150 155 160

Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn
 180

<210> 983

<211> 957

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

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cgctgcagga actcgaccac gcagtcaagg cttaagccct atg aca ttc ggc gag 115
 Met Thr Phe Gly Glu
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val
 135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln
 150 155 160 165

 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala
 170 175 180

 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly
 185 190 195

 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu
 200 205 210

 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala
 215 220 225

 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro
 230 235 240 245

 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met
 250 255 260

 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg
 265 270 275

 tca tagtcgcgga aacggccctt aat 957
 Ser

<210> 984

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 984

Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg
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 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly
 20 25 30

 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val
 35 40 45

 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe
 50 55 60

 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile
 65 70 75 80

 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg
 85 90 95

Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp
 100 105 110
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu
 115 120 125
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly
 130 135 140
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu
 145 150 155 160
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile
 165 170 175
 Val Asp Gln Ala Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys
 180 185 190
 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro
 195 200 205
 Arg Leu Ser Thr Leu Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala
 210 215 220
 Gln Gly Gly Thr Ala Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala
 225 230 235 240
 His Leu Ala Phe Pro Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro
 245 250 255
 Asp Ile Ala Glu Met Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe
 260 265 270
 Pro Gly Phe Pro Arg Ser
 275

<210> 985
 <211> 852
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(829)
 <223> RXN01892

<400> 985
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 aaagcgggttg gcacaacccc tactgaagga gaacaccact gtg acc acc tcg agt 115
 Val Thr Thr Ser Ser
 1 5
 gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163
 Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly
 10 15 20
 gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211
 Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp
 25 30 35

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aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att 259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile
      40                      45                      50

gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag 307
Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln
      55                      60                      65

cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc 355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly
      70                      75                      80                      85

aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc 403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly
                      90                      95                      100

gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa 451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu
                      105                      110                      115

cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt 499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val
                      120                      125                      130

gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc 547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr
                      135                      140                      145

act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg 595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met
150                      155                      160                      165

gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca 643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro
                      170                      175                      180

gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag 691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys
                      185                      190                      195

ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac 739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn
200                      205                      210

aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct 787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala
215                      220                      225

cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
230                      235                      240

tgatacattt agtcttataa aca 852

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<210> 986

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 986

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 Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys
 35 40 45
 Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg
 50 55 60
 Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr
 65 70 75 80
 Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe
 85 90 95
 Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
 100 105 110
 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
 115 120 125
 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
 130 135 140
 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
 145 150 155 160
 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
 165 170 175
 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
 210 215 220
 Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu
 225 230 235 240
 Val Glu Ser

<210> 987

<211> 798

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (47) .. (775)

<223> FRXA01892

<400> 987

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Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu
5 10 15 20

ggg gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154
Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val
25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202
Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu
40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250
Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu
55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298
Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu
70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346
Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His
85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394
Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala
105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442
Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg
120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490
Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp
135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538
Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu
150 155 160

atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586
Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn
165 170 175 180

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634
Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu
185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682
Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp
200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730
Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile
215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
 230 235 240

tgatacattt agtcttataa aca

798

<210> 988

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met
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Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp
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Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu
 225 230 235 240

Val Glu Ser


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<210> 989
<211> 798
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(775)  
<223> RXA00105
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				Met	Thr	Val	Pro	Thr										
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cct	tat	gaa	gac	ctt	ctt	cgg	aag	att	gct	gaa	gaa	ggg	tcc	cac	aag	163		
Pro	Tyr	Glu	Asp	Leu	Leu	Arg	Lys	Ile	Ala	Glu	Glu	Gly	Ser	His	Lys			
				10					15						20			
gac	gac	cgc	acc	ggc	acc	ggc	act	act	tct	tta	ttc	gga	caa	caa	atc	211		
Asp	Asp	Arg	Thr	Gly	Thr	Gly	Thr	Thr	Ser	Leu	Phe	Gly	Gln	Gln	Ile			
			25					30					35					
cgc	ttt	gat	ctc	aat	gaa	ggt	ttt	ccc	ctt	ctg	acc	acc	aag	aag	gtc	259		
Arg	Phe	Asp	Leu	Asn	Glu	Gly	Phe	Pro	Leu	Leu	Thr	Thr	Lys	Lys	Val			
		40					45					50						
cat	ttc	cac	tct	gtt	gtg	ggt	gag	ctt	ttg	tgg	ttc	ctt	cag	ggg	gat	307		
His	Phe	His	Ser	Val	Val	Gly	Glu	Leu	Leu	Trp	Phe	Leu	Gln	Gly	Asp			
	55					60					65							
tcc	aac	gtc	aaa	tgg	ctg	cag	gat	aac	aac	atc	cgc	att	tgg	aat	gaa	355		
Ser	Asn	Val	Lys	Trp	Leu	Gln	Asp	Asn	Asn	Ile	Arg	Ile	Trp	Asn	Glu			
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Trp	Ala	Asp	Glu	Asp	Gly	Glu	Leu	Gly	Pro	Val	Tyr	Gly	Val	Gln	Trp			
				90				95					100					
cgt	tct	tgg	cca	acc	cct	gat	ggt	cgt	cac	att	gac	cag	atc	tca	ggt	451		
Arg	Ser	Trp	Pro	Thr	Pro	Asp	Gly	Arg	His	Ile	Asp	Gln	Ile	Ser	Gly			
			105					110					115					
gct	tta	gaa	act	ctg	cga	aac	aac	cct	gat	tca	cgt	cgc	aat	att	gtc	499		
Ala	Leu	Glu	Thr	Leu	Arg	Asn	Asn	Pro	Asp	Ser	Arg	Arg	Asn	Ile	Val			
		120					125					130						
tcg	gcg	tgg	aat	gtt	tcc	gag	ctt	gaa	aac	atg	gct	ctt	ccc	cct	tgt	547		
Ser	Ala	Trp	Asn	Val	Ser	Glu	Leu	Glu	Asn	Met	Ala	Leu	Pro	Pro	Cys			
	135					140					145							
cac	ttg	ctt	ttc	cag	ctc	tat	gtc	gcc	gat	ggc	aaa	ctg	tct	tgc	cag	595		
His	Leu	Leu	Phe	Gln	Leu	Tyr	Val	Ala	Asp	Gly	Lys	Leu	Ser	Cys	Gln			
150					155					160					165			
ctc	tac	cag	cgt	tct	gcg	gac	atg	ttc	ctg	ggt	gtg	cct	ttc	aac	atc	643		
Leu	Tyr	Gln	Arg	Ser	Ala	Asp	Met	Phe	Leu	Gly	Val	Pro	Phe	Asn	Ile			
				170					175					180				

gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu
 185 190 195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp
 200 205 210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg
 215 220 225

cctacccac ctt 798

<210> 990

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 990

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Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu
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Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu
 35 40 45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp
 50 55 60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile
 65 70 75 80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val
 85 90 95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile
 100 105 110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser
 115 120 125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met
 130 135 140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly
 145 150 155 160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly
 165 170 175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala
 180 185 190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp
 195 200 205

Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210 215 220

Arg
225

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<213> Corynebacterium glutamicum

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<223> RXA00131

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Met Ile Val Ser Ile
1 5
gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr
10 15 20
cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser
25 30 35
att cac gcc caa ttg gcc gcg gaa gca ctc cac gcc cgc atg gcc gac 259
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp
40 45 50
ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg
55 60 65
cac ttc gcg att gat gac tta aat gcg ccc gcc gtg gtg ctg ctc gac 355
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp
70 75 80 85
cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp
90 95 100
gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly
105 110 115
ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val
120 125 130
gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547
Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala
135 140 145
cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

150 155 160 165
 cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg 643
 His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val
 170 175 180
 gtt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa 691
 Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu
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 ttc ctg ggt act ata aac taatcccaat tagcaggaag gat 732
 Phe Leu Gly Thr Ile Asn
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<210> 992

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 992

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 35 40 45
 Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu
 50 55 60
 Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly
 65 70 75 80
 Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala
 85 90 95
 Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu
 100 105 110
 Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp
 115 120 125
 Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu
 130 135 140
 Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln
 145 150 155 160
 Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu
 165 170 175
 Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala
 180 185 190
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Met Thr Glu Arg Thr																
1 5																
ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa																163
Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu																
10 15 20																
atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat																211
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp																
25 30 35																
ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac																259
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His																
40 45 50																
gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca																307
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala																
55 60 65																
cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg																355
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp																
70 75 80 85																
cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc																403
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly																
90 95 100																
acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac																451
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His																
105 110 115																
ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc																499
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe																
120 125 130																
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Pro Asn Leu																
135																

<400> 994
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Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys	35	40	45
His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu	50	55	60
Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg	65	70	75
Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala	85	90	95
Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly	100	105	110
Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu	115	120	125
Ile Ser Ile Trp Phe Pro Asn Leu	130	135	

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<211> 831

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(808)

<223> RXA00718

<400> 995

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                               Val Thr Glu Ile Ser
                               1 5
aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
                               10 15 20
acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
                               25 30 35
aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259
Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
                               40 45 50
ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
                               55 60 65
acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355

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Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp Pro Ala Ser Thr Glu
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 Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp Ile Arg Gly Pro Glu
 90 95 100
 gtc acc caa aat gtc tcc gca gtg tcc gcg atc cct gag gtt cgt gaa 451
 Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile Pro Glu Val Arg Glu
 105 110 115
 aac ttg gtg gcg ttg cag cgc gca ctc gcc gcc aaa gca cat cgc tgc 499
 Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala Lys Ala His Arg Cys
 120 125 130
 gtc gtc gaa ggc aga gac atc gga acg gca gtg ctt gtc gac gcg ccc 547
 Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val Leu Val Asp Ala Pro
 135 140 145
 atc aag gcg ttt ctc acc gcc tca gcg gaa gtc cgc gcc cag cga cgc 595
 Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val Arg Ala Gln Arg Arg
 150 155 160 165
 ttt gac caa gac acc gca gca ggt cgc gac gta gat ttc gac gct gtg 643
 Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val Asp Phe Asp Ala Val
 170 175 180
 ctg gca gat gtt gtt cgc cgc gat gaa cta gat tcc acc cgt gcc gcc 691
 Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp Ser Thr Arg Ala Ala
 185 190 195
 tca ccg ctg aaa cca gca gat gat gca cac atc gtg gac acc tct gat 739
 Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile Val Asp Thr Ser Asp
 200 205 210
 atg acc atg gat caa gta ctt gat cac ctc atc cac cta gtg gaa gcc 787
 Met Thr Met Asp Gln Val Leu Asp His Leu Ile His Leu Val Glu Ala
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 Ser Ala Glu Arg Ser Asn Gln
 230 235

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 <211> 236
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 996
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 35 40 45
 Ala Thr Leu His Val Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala
 50 55 60

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp
 65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp
 85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile
 100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala
 115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val
 130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val
 145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val
 165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp
 180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile
 195 200 205

Val Asp Thr Ser Asp Met Thr Met Asp Gln Val Leu Asp His Leu Ile
 210 215 220

His Leu Val Glu Ala Ser Ala Glu Arg Ser Asn Gln
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<210> 997

<211> 1785

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1762)

<223> RXA01599

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 Met Thr Ser Ser Arg
 1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163
 Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser
 10 15 20

tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211
 Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile
 25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

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Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
	55					60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
70					75					80					85	
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Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
				90				95						100		
gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggt	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
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Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
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Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
	135					140					145					
gtg	atc	tct	gag	gtc	ggc	ggc	acc	gtc	ggc	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
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Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
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tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggt	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190					195			
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205					210				
atc	ggt	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
	215					220					225					
cct	caa	ggt	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	gtt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
230					235					240					245	
gaa	ggc	gtt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
				250				255						260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
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Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	

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Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly		
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1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val		
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1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile		
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1171		
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser		
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1219		
Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile		
	360	365 370
gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg		
1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro		
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ctt ctt ggc cta tgc ctt ggc ctg cag tgc acc gtc atc gag gca gca		
1315		
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390	395	400 405
cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct		
1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala		
	410	415 420
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg		
1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val		
	425	430 435
tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct		
1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro		
	440	445 450
gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg		
1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr		
	455	460 465
gaa gtc tcc gag cgc cac cgt cac cgc tat gag gtc aat aat gcc tac		
1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr		
470	475	480 485

cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca
1603

Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser
490 495 500

cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat
1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His
505 510 515

cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca
1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro
520 525 530

acc cat gct cat cca ctg ttt tac ggc ctg gtg aag acc gct ttg gag
1747

Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu
535 540 545

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1785

Leu Arg Val His Pro
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<210> 998

<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 998

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Gly Gln Leu Leu Ile Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu
35 40 45

Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His
50 55 60

Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu
65 70 75 80

Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn
85 90 95

Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg
100 105 110

Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

145	150	155	160
Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu	165	170	175
Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr	180	185	190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val	195	200	205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg	210	215	220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met	225	230	235
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser	245	250	255
Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe	260	265	270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr	275	280	285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr	290	295	300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser	305	310	315
Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr	325	330	335
Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala	340	345	350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe	355	360	365
Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg	370	375	380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr	385	390	395
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr	405	410	415
Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu	420	425	430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg	435	440	445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu	450	455	460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu	465	470	475
			480

Val Asn Asn Ala Tyr Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val
 485 490 495

Phe Ser Gly Thr Ser Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr
 500 505 510

Pro Lys Glu Val His Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu
 515 520 525

Tyr Lys Ser Arg Pro Thr His Ala His Pro Leu Phe Tyr Gly Leu Val
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Lys Thr Ala Leu Glu Leu Arg Val His Pro
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<210> 999

<211> 3462

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(3439)

<223> RXN02234

<400> 999

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 Met Pro Lys Arg Ser
 1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163
 Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly
 10 15 20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211
 Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu
 25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acc 259

Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr
 40 45 50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307
 Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile
 55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355
 Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly
 70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403
 His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu
 90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451
 Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly
 105 110 115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499
 Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp
 120 125 130

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547
 Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala
 135 140 145

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595
 Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala
 150 155 160 165

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643
 Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly
 170 175 180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691
 Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala
 185 190 195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739
 Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu
 200 205 210

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr
 215 220 225

gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835
 Ala Asp Asn Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg
 1027
 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc
 1075
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc
 1123
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac
1171

Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp
345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc
1219

Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly
360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg
1267

Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met
375 380 385

tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc
1315

Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser
390 395 400 405

ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc
1363

Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe
410 415 420

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag
1411

Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys
425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt
1459

Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu
440 445 450

ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg
1507

Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp
455 460 465

ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt
1555

~~Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val~~
470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg
1603

Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met
490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc
1651

Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly
505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta
1699

Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val
520 525 530

ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg
1747

Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro
535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc
1795

Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val
550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca
1843

Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro
570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca
1891

Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala
585 590 595

gct ctt gag ctg tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc
1939

Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys
600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac
1987

Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr
615 620 625

ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag
2035

Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu
630 635 640 645

gcg cag tcc ggc acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag
2083

Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln
650 655 660

act cct ctg ggc ttg gca gat cgt ttg aag aag gct ggc gtc cct gtc
2131

Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val
665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag
2179

Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu
680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc
2227

Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly
695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc
2275

Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser
710 715 720 725

tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg
2323

Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met
730 735 740

gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca
2371

Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala
745 750 755

act gag ttg tct tct gac cac cca gtg ctg gtt gac cgc ttc cta gac
2419

Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp
760 765 770

aac gct att gag atc gac gtc gac gca ctg tgc gac ggc gac gag gtc
2467

Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val
775 780 785

tac ctg gca ggc gtc atg gag cac atc gag gaa gcc ggc att cac tcc
2515

Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser
790 795 800 805

ggg gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac
2563

Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp
810 815 820

atc gag aag gtc cgc gaa gca acc aag aag ctg gct ctg ggc atc ggt
2611

Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly
825 830 835

gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc
2659

Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu
840 845 850

tac gtc atc gag gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc
2707

~~Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val~~
855 860 865

tcc aag gca acg ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca
2755

Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala
870 875 880 885

gtg ggc gcc acc atc aag gat ctc caa gat gag ggc atg att cct acc
2803

Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr
890 895 900

gag tac gac ggc ggc tcc ttg cca ctg gac gct cca atc gct gtg aag
2851

Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys
905 910 915

gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc
2899

Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr
920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg
2947

Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met
935 940 945

ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc
2995

Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly
950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct
3043

Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala
970 975 980

aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg
3091

Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu
985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc
3139

Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg
1000 1005 1010

cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc
3187

Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg
1015 1020 1025

gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa
3235

Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu
1030 1035 1040 1045

gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac
3283

Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His
1050 1055 1060

gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg
3331

Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu
1065 1070 1075

atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc
3379

Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala
1080 1085 1090

ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac
3427

Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His
1095 1100 1105

gca gtc aag gct taagccctat gacattcggc gag

3462

Ala Val Lys Ala

1110

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<211> 1113

<212> PRT

<213> Corynebacterium glutamicum

<400> 1000

Met Pro Lys Arg Ser Asp Ile Asn His Val Leu Val Ile Gly Ser Gly
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Pro Ile Val Ile Gly Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln
20 25 30

Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn
35 40 45

Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr
50 55 60

Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys
65 70 75 80

Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly
85 90 95

Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile
100 105 110

Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile
115 120 125

Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile
130 135 140

Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val
145 150 155 160

~~His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser~~
~~165 170 175~~

Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
180 185 190

Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn
195 200 205

Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu
210 215 220

Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu
225 230 235 240

Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala
245 250 255

Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln

260	265	270
Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn		
275	280	285
Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu		
290	295	300
Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr		
305	310	315
Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr		
325	330	335
Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe		
340	345	350
Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe		
355	360	365
Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser		
370	375	380
Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn		
385	390	395
Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys		
405	410	415
Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val		
420	425	430
Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu		
435	440	445
Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser		
450	455	460
Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe		
465	470	475
Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg		
485	490	495
Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg		
500	505	510
Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu		
515	520	525
Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe		
530	535	540
Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala		
545	550	555
Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile		
565	570	575
Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr		
580	585	590

Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
 595 600 605
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
 610 615 620
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu
 625 630 635 640
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val
 645 650 655
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys
 660 665 670
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala
 675 680 685
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro
 690 695 700
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val
 705 710 715 720
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu
 725 730 735
 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp
 740 745 750
 Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val
 755 760 765
 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys
 770 775 780
 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu
 785 790 795 800
 Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr
 805 810 815
 Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu
 820 825 830
 Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu
 835 840 845
 Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg
 850 855 860
 Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala
 865 870 875 880
 Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu
 885 890 895
 Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala
 900 905 910

Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg
 915 920 925

Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser
 930 935 940

Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala
 945 950 955 960

Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val
 965 970 975

Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile
 980 985 990

Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr
 995 1000 1005

Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys
 1010 1015 1020

Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg
 1025 1030 1035 1040

Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser
 1045 1050 1055

Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr
 1060 1065 1070

Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val
 1075 1080 1085

Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu
 1090 1095 1100

Gln Glu Leu Asp His Ala Val Lys Ala
 1105 1110

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 <211> 3221
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 <222> (1)..(3198)
 <223> FRXA02234

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 Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His
 1 5 10 15

acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct 96
 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
 20 25 30

aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt 144
 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu

35				40				45								
ggt	ggc	cag	act	gca	ctt	aac	gca	gct	atc	cag	ctg	gat	cgc	ctc	ggc	192
Gly	Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	
50						55				60						
atc	ctg	gaa	aag	tac	ggc	gtt	gaa	ctc	atc	ggt	gca	gac	atc	gat	gcc	240
Ile	Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	
65				70						75				80		
att	gag	cgc	ggc	gaa	gat	cgc	cag	aag	ttc	aag	gat	att	gtc	acc	acc	288
Ile	Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	
				85				90						95		
atc	ggt	ggc	gaa	tcc	gcg	cgt	tcc	cgc	gtc	tgc	cac	aac	atg	gaa	gaa	336
Ile	Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	
			100				105						110			
gtc	cac	gag	act	gtc	gca	gaa	ctc	ggc	ctt	cca	gta	gtc	gtg	cgt	cca	384
Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	
		115				120						125				
tcc	ttc	act	atg	ggt	ggc	ctg	ggc	tcc	ggt	ctt	gca	tac	aac	acc	gaa	432
Ser	Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	
130						135				140						
gac	ctt	gag	cgc	atc	gct	ggt	ggc	gga	ctt	gct	gca	tct	cct	gaa	gca	480
Asp	Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	
145				150						155				160		
aac	gtc	ttg	atc	gaa	gaa	tcc	atc	ctt	ggt	tgg	aag	gaa	ttc	gag	ctc	528
Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	
				165				170						175		
gag	ctc	atg	cgc	gat	acc	gca	gac	aac	gtt	gtg	gtt	atc	tgc	tcc	att	576
Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	
			180				185						190			
gaa	aac	gtc	gac	gca	ctg	ggc	gtg	cac	acc	ggc	gac	tct	gtc	acc	gtg	624
Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	
		195				200						205				
gca	cct	gcc	ctg	acc	ctg	act	gac	cgt	gaa	ttc	cag	aag	atg	cgc	gat	672
Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	
210						215				220						
cag	ggt	atc	gcc	atc	atc	cgc	gag	gtc	ggc	gtg	gac	acc	ggt	gga	tgt	720
Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	
225				230						235				240		
aac	atc	cag	ttc	gcc	atc	aac	cca	gtt	gat	ggc	cgc	atc	atc	acc	att	768
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	
				245				250						255		
gag	atg	aac	cca	cgt	gtg	tct	cgt	tcc	tcc	gct	ctg	gca	tcc	aag	gca	816
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	
			260				265						270			
acg	ggc	ttc	cca	att	gcc	aag	atg	gct	gcc	aag	ctg	gct	atc	gga	tac	864
Thr	Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	
		275				280						285				

acc ctg gat gag atc acc aac gac atc act ggt gaa acc cca gct gcg 912
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
 290 295 300

ttt gag ccc acc atc gac tac gtc gtg gtc aag gcc cca cgc ttt gct 960
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
 305 310 315 320

ttc gag aag ttt gtc ggc gct gat gac act ttg acc acc acc atg aag
 1008
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335

tcc gtc ggt gag gtc atg tcc ctg ggc cgc aac tac att gca gca ctg
 1056
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
 340 345 350

aac aag gca ctg cgt tcc ctg gaa acc aag cag cag ggt ttc tgg acc
 1104
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365

aag cct gat gag ttc ttc gca ggg gag cgc gct acc gat aag gca gct
 1152
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380

gtt ctg gaa gat ctc aag cgc cca acc gaa ggc cgc ctc tac gac gtt
 1200
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400

gag ctg gca atg cgc ctt ggc gca agc gtg gaa gaa ctc tac gaa gca
 1248
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415

tct tct att gat cct tgg ttc ctc gcc gag ctt gaa gct ctc gtg cag
 1296
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430

ttc cgc cag aag ctc gtt gac gca cca ttc cta aac gaa gat ctc ctg
 1344
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
 435 440 445

cgc gaa gca aag ttc atg ggt ctg tcc gac ctg cag atc gca gcc ctt
 1392
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460

cgc cca gag ttc gct ggc gaa gac ggc gta cgc acc ttg cgt ctg tcc
 1440
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480

cta ggc atc cgc cca gta ttc aag act gtg gat acc tgt gca gca gag
 1488

Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
485 490 495

ttt gaa gct aag act ccg tac cac tac tcc gca tac gag ctg gat cca
1536

Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
500 505 510

gca gct gag tct gag gtc gca cca cag act gag cgt gaa aag gtc ctg
1584

Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
515 520 525

atc ttg ggc tcc ggt cca aac cgc atc ggc cag ggc atc gag ttc gac
1632

Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
530 535 540

tac tcc tgt gtt cac gca gct ctt gag ctg tcc cgc gtc ggc tac gaa
1680

Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
545 550 555 560

act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac
1728

Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
565 570 575

acc gct gac cgc ctg tac ttc gag cca ctg acc ttc gaa gac gtc atg
1776

Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
580 585 590

gag gtc tac cac gct gag gcg cag tcc ggc acc gtc gca ggt gtt atc
1824

Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile
595 600 605

gtc cag ctt ggt ggc cag act cct ctg ggc ttg gca gat cgt ttg aag
1872

Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys
610 615 620

aag gct ggc gtc cct gtc att ggt acc tcc cca gag gca atc gac atg
1920

Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met
625 630 635 640

gct gag gac cgt ggc gag ttc ggt gca ctg ctg aac cgc gag cag ctt
1968

Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu
645 650 655

cct gct cca gca ttc ggc acc gca acc tct ttc gaa gag gct cgc aca
2016

Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
660 665 670

gta gcc gat gag atc agc tac cca gtg ctg gtt cgc cct tcc tac gtc
2064

Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val

675	680	685
ttg ggt ggc cgt ggc atg gag att gtc tac gat gag gct tcc ctc gag 2112		
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu 690 695 700		
gat tac atc aac cgc gca act gag ttg tct tct gac cac cca gtg ctg 2160		
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu 705 710 715 720		
gtt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg 2208		
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu 725 730 735		
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag 2256		
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740 745 750		
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg 2304		
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met 755 760 765		
act ttg ggc gca cag gac atc gag aag gtc cgc gaa gca acc aag aag 2352		
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys 770 775 780		
ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca 2400		
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala 785 790 795 800		
ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc 2448		
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser 805 810 815		
cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag 2496		
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys 820 825 830		
gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat 2544		
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp 835 840 845		
gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac 2592		
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp 850 855 860		
gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt 2640		
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg 865 870 875 880		

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag
2688

Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
885 890 895

tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat
2736

Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc
2784

Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca
2832

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc
2880

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala
1060 1065

gag
3221

<210> 1002

<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 1002

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Thr	Tyr	Val	Glu	Pro	Ile	Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala
			20					25					30		
Lys	Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu
	35						40					45			
Gly	Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly
	50					55					60				
Ile	Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala
65					70					75					80
Ile	Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr
				85					90					95	
Ile	Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu
			100					105					110		
Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro
			115				120					125			
Ser	Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu
	130					135					140				
Asp	Leu	Gln	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala
145					150				155					160	
Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu
				165					170					175	
Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile
			180					185					190		
Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val
			195				200					205			
Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp
	210					215					220				
Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys
225					230					235					240
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile
			245						250					255	
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala
			260					265						270	

Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr
 275 280 285
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
 290 295 300
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
 305 310 315 320
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
 340 345 350
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
 435 440 445
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
~~Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro~~
~~500 505 510~~
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
 565 570 575
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
 580 585 590
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile

595	600	605
Val Gln Leu Gly Gly Gln Thr 610	Pro Leu Gly Leu Ala 615	Asp Arg Leu Lys 620
Lys Ala Gly Val Pro Val Ile Gly Thr Ser 625	Pro Glu Ala Ile Asp Met 630	635
Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu 645	650	655
Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr 660	665	670
Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val 675	680	685
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu 690	695	700
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu 705	710	715
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu 725	730	735
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740	745	750
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met 755	760	765
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys 770	775	780
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala 785	790	795
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser 805	810	815
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys 820	825	830
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp 835	840	845
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp 850	855	860
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg 865	870	875
Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys 885	890	895
Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr 900	905	910
Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr 915	920	925

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
 1010 1015 1020

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
 1025 1030 1035 1040

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055

Leu Gln Glu Leu Asp His Ala Val Lys Ala
 1060 1065

<210> 1003

<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> RXN00450

<400> 1003

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~~gttttgataa tgatctgggt cggggtgggg gattcgacta gtg ggc gtt tta cct 115~~

Val Gly Val Leu Pro

1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163

Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211

Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val

25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259

Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg

40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307

Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg

55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga cgc atc 424
 Gly Ala Arg Ile Gly Arg Ile
 105

<210> 1004

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
 100 105

<210> 1005

<211> 418

<212> DNA

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<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1005

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 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

	10	15	20	
gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc				211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val				
	25	30	35	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga				259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
	40	45	50	
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga				307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
	70	75	80	85
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
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Gly Ala Arg Ile Gly				
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<211> 106

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<213> Corynebacterium glutamicum

<400> 1006

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Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr				
35	40	45		

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu				
50	55	60		

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg				
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Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys				
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Ala Gly Ala Leu Val Gly Ala Arg Ile Gly		
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<222> (101)..(1345)

<223> RXN02272

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Val Arg Ile Thr Asn
1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
55 60 65

cct cgc gaa aac tct tcc gcc aca ctt ttt gaa gcc atc gaa atc tgg 355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
70 75 80 85

gcc gac cgc aag acc caa gcc ttc cac atc aaa gaa gac att aaa gcg 403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
90 95 100

aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac gcc gtt ggt ttc 451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
120 125 130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
135 140 145

att gtc gcc ttc ccg caa aat gcc att tac gcc tac gaa ggt gcc cag 595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt gcc 643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
170 175 180

atc cca cac ctt gaa ccc acc cga gac gat gcc gtc gag tcg gtg aaa 691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His

200	205	210	
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Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala			
215	220	225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat			835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His			
230	235	240	245
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta			883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu			
250	255	260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa			931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu			
265	270	275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt			979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly			
280	285	290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt			
1027			
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe			
295	300	305	
tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat			
1075			
Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp			
310	315	320	325
cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca			
1123			
Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr			
330	335	340	
gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc			
1171			
Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala			
345	350	355	
gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg			
1219			
Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala			
360	365	370	
aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga			
1267			
Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg			
375	380	385	
aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc			
1315			
Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser			
390	395	400	405
agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc			
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410	415		

ctt
1368

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35 40 45
Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60
Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80
Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
85 90 95
Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
100 105 110
His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
115 120 125
Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
130 135 140
Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
145 150 155 160
Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
165 170 175
Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
180 185 190
Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
195 200 205
Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
210 215 220
Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
225 230 235 240
Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
245 250 255
Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
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Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
 385 390 395 400

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Val Arg Ile Thr Asn

1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163

Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly

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gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211

Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp

25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259

His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln

40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307

Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile

55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355
 Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
 70 75 80 85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403
 Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
 90 95 100

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 Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
 105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
 Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
 120 125 130

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 Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
 135 140 145

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 Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
 150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643
 Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
 170 175 180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691
 Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
 185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739
 Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His
 200 205 210

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 Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala
 215 220 225

gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat 835
 Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His
 230 235 240 245

tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta 883
 Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu
 250 255 260

ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa 931
 Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu
 265 270 275

aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt 979
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 280 285 290

gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt
 1027
 Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe
 295 300 305

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat
1075

Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp
310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca
1123

Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr
330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc
1171

Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala
345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg
1219

Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala
360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga
1267

Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg
375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc
1315

Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser
390 395 400 405

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1365

Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
410 415

ctt
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20 25 30

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35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
 85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
 100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
 370 375 380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
 385 390 395 400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

405

410

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 20 25 30

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 35 40 45

Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val
 50 55 60

Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val
 65 70 75 80

Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly
 85 90 95

Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His
 100 105 110

Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu
 115 120 125

Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met
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Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
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 Leu Glu Leu Asn Lys
 1 5

gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163
 Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly
 10 15 20

tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcggtgc 212
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val
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gatttgggca caa 225

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

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Ala Val

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<212> DNA

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 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt gcc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
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 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
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 Met Asp Ile Thr Ile
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 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
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 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35
 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50
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 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85
 gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
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 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
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 gac gca ttg acc gaa tct 613

Asp Ala Leu Ala Glu Ser
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35 40 45
Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
50 55 60
Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
65 70 75 80
Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
85 90 95
Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
100 105 110
Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
115 120 125
Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
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Val Ser Glu Gln Ala
1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg
 10 15 20

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 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr
 25 30 35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met
 40 45 50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp
 55 60 65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu
 70 75 80 85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val
 90 95 100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro
 105 110 115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp
 120 125 130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu
 135 140 145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595
 Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro
 150 155 160 165

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 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val
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Phe Glu Asp Leu Thr Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala
 35 40 45
 Val Val Asp Ala Met Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile
 50 55 60
 Ile Gly Gly Leu Asp Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala
 65 70 75 80
 Tyr Lys Leu Gly Leu Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu
 85 90 95
 Pro Pro Pro Val Val Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala
 100 105 110
 Ala Leu Glu Leu Pro Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile
 115 120 125
 Val Leu Ile Asp Asp Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala
 130 135 140
 Arg Lys Leu Ile Glu Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu
 145 150 155 160
 Ala Ile Glu Val Pro Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg
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 Pro Val Ile Val Val Arg Asp Pro Gln
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 Met Ser Asn Asn Val
 1 5
 gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163
 Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly
 10 15 20
 acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211
 Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg
 25 30 35
 atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259
 Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu
 40 45 50
 gaa gac ctc atc ctg gtg tgc gtg ctc aag gcc gcg ttc tac ttc ctg 307

Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly Ala Phe Tyr Phe Leu
 55 60 65
 gca gat ttc tcc cgc atg ctc gac atc ccc acc cag tcc gag ttc atg 355
 Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met
 70 75 80 85
 gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403
 Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg
 90 95 100
 atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451
 Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile
 105 110 115
 gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499
 Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg
 120 125 130
 aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547
 Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu
 135 140 145
 cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595
 Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly
 150 155 160 165
 ttt gat att cca aat gag ttt gtt gtg ggc tac gga ctt gat ttc gca 643
 Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala
 170 175 180
 gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691
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 Tyr Ser Asp
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<210> 1022

<211> 200

<212> PRI

<213> Corynebacterium glutamicum

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 Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu
 35 40 45
 Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly
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 Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr
 65 70 75 80

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													Met	Thr	Glu	Glu	Arg				
													1					5			
gag	att	ctg	acc	tat	gag	atg	ttc	gga	aca	gca	atg	cgg	gag	ctg	gcc		16				
Glu	Ile	Leu	Thr	Tyr	Glu	Met	Phe	Gly	Thr	Ala	Met	Arg	Glu	Leu	Ala						
				10					15					20							
caa	gaa	att	att	gat	gac	tac	cag	cca	gat	tgc	gtg	ctg	tcc	att	gcg		21				
Gln	Glu	Ile	Ile	Asp	Asp	Tyr	Gln	Pro	Asp	Cys	Val	Leu	Ser	Ile	Ala						
				25					30					35							
cgt	ggt	ggt	ctt	cta	atc	ggt	ggc	gca	ctt	ggt	tat	gcg	ctg	ggt	atc		25				
Arg	Gly	Gly	Leu	Leu	Ile	Gly	Gly	Ala	Leu	Gly	Tyr	Ala	Leu	Gly	Ile						
				40					45					50							
aag	aat	gta	tcg	gtg	atc	aat	gtg	gag	ttc	tac	acc	gat	att	gga	gag		30				
Lys	Asn	Val	Ser	Val	Ile	Asn	Val	Glu	Phe	Tyr	Thr	Asp	Ile	Gly	Glu						
				55					60					65							
cac	ttg	gag	gag	cca	atg	atg	ctg	cct	cca	act	cca	aaa	gct	gtt	gat		35				
His	Leu	Glu	Glu	Pro	Met	Met	Leu	Pro	Pro	Thr	Pro	Lys	Ala	Val	Asp						
70					75					80					85						

ctc tgc gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403
 Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp Val Ala Asp Thr Gly
 90 95 100

aag act ctt gag ttg gtc agg gac ttc ctg ggt gac caa gtt gtc gaa 451
 Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu
 105 110 115

gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499
 Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro
 120 125 130

gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547
 Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser
 135 140 145

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 Thr Leu Pro Pro Val Glu Pro Ser Lys
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tgc 597

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<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 1024

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 20 25 30

Val Leu Ser Ile Ala Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly
 35 40 45

Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr
 50 55 60

Thr Asn Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr
 65 70 75 80

Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp
 85 90 95

Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly
 100 105 110

Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn
 115 120 125

Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile
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Asn Phe Pro Trp Ser Thr Leu Pro Pro Val Glu Pro Ser Lys
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 <223> RXA00981

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 Met Ser Glu Asn Leu
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cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag 163
 Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys
 10 15 20

aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc 211
 Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly
 25 30 35

att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc 259
 Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser
 40 45 50

cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag 307
 Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys
 55 60 65

aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc 355
 Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu
 70 75 80 85

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga 403
 Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
 90 95 100

atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg 451
 Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
 105 110 115

acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct 499
 Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
 120 125 130

aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg 547
 Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
 135 140 145

cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag 595
 Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
 150 155 160 165

atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc 643
 Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
 170 175 180

tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
 185 190 195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
 200 205 210

gttgaaacca ctg 753

<210> 1026

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1026

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Ile Gln Met Ile Lys Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu
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Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
 35 40 45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
 50 55 60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
 180 185 190

Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
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Val Thr
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                                         Met Ser Leu Glu Arg
                                         1           5

aac aca caa aaa tct tcc atg ggt gtg cga agc atg tca gcc agg ctt 163
Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
                        10                15                20

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 211
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                        25                30                35

ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
                        40                45                50

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
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att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                        70                75                80                85

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 403
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                        90                95                100

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 451
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                        105                110                115

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 499
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                        120                125                130

aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 547
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                        135                140                145

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 595
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                        150                155                160                165

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 643
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
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ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
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Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
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gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 787
Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
      215                      220                      225

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 835
Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
      230                      235                      240                      245

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 883
Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
      250                      255                      260

gaa gtg ctt ggt cga cca aag cac tac tgg tct atc tat caa aag atg 931
Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met
      265                      270                      275

atc gtt cgc ggt cgt gat ttt gac gat att ttt gat ctt gtt ggc atc 979
Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile
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cgc atc ctg gta gac aac gtg aac aac tgt gta cgc cgc cat cgg tgt
1027
Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val Arg Arg His Arg Cys
      295                      300                      305

cgt gca ctc cct gtt caa tgc tct gcc tgg ccg att caa aga cta tat
1075
Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro Ile Gln Arg Leu Tyr
      310                      315                      320                      325

ttc agc ccc gcg ctt cgg tgt cta cca atc cct gca cac cac cgt gat
1123
Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro Ala His His Arg Asp
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1158
Gly Thr Trp Arg
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<212> PRT

<213> Corynebacterium glutamicum

<400> 1028

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Met Ser Ala Arg Leu Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr
      20                      25                      30

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Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro

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 Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
 65 70 75 80
 Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
 85 90 95
 Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
 100 105 110
 Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
 115 120 125
 Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 130 135 140
 Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
 145 150 155 160
 Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
 165 170 175
 Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 180 185 190
 Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 195 200 205
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 210 215 220
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
 225 230 235 240
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
 245 250 255
 Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser
 260 265 270
 Ile Tyr Gln Lys Met Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe
 275 280 285
 Asp Leu Val Gly Ile Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val
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 Arg Arg His Arg Cys Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro
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 Ala His His Arg Asp Gly Thr Trp Arg
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<211> 903
 <212> DNA
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<220>
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 <222> (101)..(880)
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                                         Met Ser Ala Arg Leu
                                         1                               5

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 163
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                        10                        15                        20

ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 211
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
                        25                        30                        35

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 259
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
                        40                        45                        50

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 307
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                        55                        60                        65

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 355
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                        70                        75                        80                        85

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 403
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                        90                        95                        100

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 451
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                        105                        110                        115

aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 499
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                        120                        125                        130

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 547
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                        135                        140                        145

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 595
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
                        150                        155                        160                        165

ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 643
Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
                        170                        175                        180

cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 691

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Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
 185 190 195

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 739
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
 200 205 210

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
 215 220 225

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
 230 235 240 245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880
 Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu Ser Phe Lys Arg
 250 255 260

tgatcgttcg cggtcgtgat ttt 903

<210> 1030

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 1030

Met Ser Ala Arg Leu Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr
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Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro
 20 25 30

Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg
 35 40 45

Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
 50 55 60

Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
 65 70 75 80

Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
 85 90 95

Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
 100 105 110

Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 115 120 125

Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
 130 135 140

Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
 145 150 155 160

Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 180 185 190
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 195 200 205
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
 210 215 220
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
 225 230 235 240
 Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Ser Gly Leu
 245 250 255
 Ser Phe Lys Arg
 260

<210> 1031
 <211> 262
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(262)
 <223> FRXA02773

<400> 1031
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 tgcttggtcg nccnaagcac tctggtcttt ctttcaaaag atg atc gtt cgc ggt 115
 Met Ile Val Arg Gly
 1 5
 cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163
 Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa
 10 15 20
 gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc ccn 211
 Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro
 25 30 35

gtn caa tgc tct gnc tgg ncg ntt caa aga cta tat ttc agc ccc gcg 259
 Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu Tyr Phe Ser Pro Ala
 40 45 50
 ctt 262
 Leu

<210> 1032
 <211> 54
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1032
 Met Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly
 1 5 10 15

Ile Arg Xaa Leu Xaa Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg
 20 25 30

Cys Arg Ala Leu Pro Val Gln Cys Ser Xaa Trp Xaa Xaa Gln Arg Leu
 35 40 45

Tyr Phe Ser Pro Ala Leu
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<210> 1033

<211> 654

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(631)

<223> RXA01835

<400> 1033

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 ttctctgcgtg aatacacttt ccccgcgccct tcgcaaagct atg aat act gcc gcg 115
 Met Asn Thr Ala Ala
 1 5
 tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
 10 15 20
 agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
 25 30 35
 gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259
 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
 40 45 50
 ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
 55 60 65
 gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
 70 75 80 85
 aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403
 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
 90 95 100
 tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
 105 110 115
 tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499
 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
 120 125 130
 ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547

Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
 135 140 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
 150 155 160 165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
 170 175

gcggcgctcga taa 654

<210> 1034

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 1034

Met Asn Thr Ala Ala Trp Ala His Arg His His Val Arg Lys Gly Gly
 1 5 10 15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala
 20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
 65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
 85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
 100 105 110

Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
 115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
 130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
 145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser
 165 170 175

Ala

<210> 1035

<211> 1395

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1372)

<223> RXA01483

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gcgtgcacgc catgagcaac ttcggaggct gaaaaagtag atg tac ccc tat tcc 115
 Met Tyr Pro Tyr Ser
 1 5

gac gca gac gct ttt cga cgc cag cct gag cgc gcc aag tcc agc caa 163
 Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg Ala Lys Ser Ser Gln
 10 15 20

ctg cgt acc agc gcc gta gac acc cgc agc gcg ttc gcc cgc gac cgg 211
 Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
 25 30 35

gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
 Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
 40 45 50

caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
 Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
 55 60 65

cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
 His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
 70 75 80 85

gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
 Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
 90 95 100

ggg cat ccg ccg tat gga cac aac ggt gaa aac gcg ttg aat gaa gtt 451
 Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
 105 110 115

gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
 Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
 120 125 130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
 Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
 135 140 145

ggg ctg aac ttg tcg ccg gct gct ctt gat gct gca tgt aag tat ccg 595
 Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
 150 155 160 165

tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct 643
 Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
 170 175 180

tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
 Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
 185 190 195

gat ctt cgc cca ccg atc gaa gcg cag gtc atg gac ttt tct gat gac 739
 Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met Asp Phe Ser Asp Asp
 200 205 210

att gcc tac tcg gtg cac gat gtg gaa gac ggt att gta tcc ggg cgt 787
 Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg
 215 220 225

atc gac tta aaa gtg ctg tgg gac ctg gtt gaa tta gca gct ttg gca 835
 Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala
 230 235 240 245

gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag 883
 Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu
 250 255 260

ggt gca gca tcg ttg cgg gaa ctt ccg gtg gtg gct gcc gct gcg gat 931
 Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Ala Asp
 265 270 275

ttt gat ttc tca ctg cgt tcc tac gct gcg ctg aag gcg atg act tca 979
 Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser
 280 285 290

gaa cta gtg gga aga tac gtt ggc tct acc atc gag tca aca aag aaa
 1027
 Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys
 295 300 305

aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att
 1075
 Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile
 310 315 320 325

cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt
 1123
 Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val
 330 335 340

ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa
 1171
 Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln
 345 350 355

cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg
 1219
 Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro
 360 365 370

gga tcg ttg gat ccg atg tat cgc cag tgg ttt att gaa gcg gat tca
 1267
 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg
 1315
 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr
 390 395 400 405

gag tct cgt ctg gaa cgc ctt gcc cgg aat gct gct gac atc tca gga
 1363

Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala Ala Asp Ile Ser Gly
 410 415 420

ttt ttg gga taattgggta gagcagcagt aag
 1395
 Phe Leu Gly

<210> 1036

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 1036

Met Tyr Pro Tyr Ser Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg
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Ala Lys Ser Ser Gln Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala
 20 25 30

Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg
 35 40 45

Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro
 50 55 60

Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly
 65 70 75 80

Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly
 85 90 95

Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn
 100 105 110

Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala
 115 120 125

Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp
 130 135 140

Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala
 145 150 155 160

Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn
 165 170 175

Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile
 180 185 190

Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met
 195 200 205

Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly
 210 215 220

Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu
 225 230 235 240

Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro

245										250					255				
Ala	Glu	Leu	Ile	Glu	Gly	Ala	Ala	Ser	Leu	Arg	Glu	Leu	Pro	Val	Val				
			260					265					270						
Ala	Ala	Ala	Ala	Asp	Phe	Asp	Phe	Ser	Leu	Arg	Ser	Tyr	Ala	Ala	Leu				
			275				280					285							
Lys	Ala	Met	Thr	Ser	Glu	Leu	Val	Gly	Arg	Tyr	Val	Gly	Ser	Thr	Ile				
	290					295					300								
Glu	Ser	Thr	Lys	Lys	Thr	His	Ala	Gly	Ile	Asp	Val	Gly	Arg	Met	His				
305					310					315					320				
Gly	Asp	Leu	Ile	Ile	Pro	Glu	Thr	Ala	Ala	Ser	Glu	Val	Lys	Leu	Leu				
			325					330					335						
Lys	Thr	Leu	Ala	Val	Leu	Tyr	Val	Met	Asp	Asp	Pro	Gly	His	Leu	Ala				
		340					345						350						
Arg	Gln	Asn	Arg	Gln	Arg	Asp	Arg	Ile	Phe	Arg	Val	Phe	Asp	Tyr	Leu				
		355					360					365							
Val	Leu	Gly	Ala	Pro	Gly	Ser	Leu	Asp	Pro	Met	Tyr	Arg	Gln	Trp	Phe				
	370					375					380								
Ile	Glu	Ala	Asp	Ser	Glu	Ser	Glu	Gln	Ile	Arg	Val	Ile	Val	Asp	Gln				
385					390					395					400				
Ile	Ala	Ser	Met	Thr	Glu	Ser	Arg	Leu	Glu	Arg	Leu	Ala	Arg	Asn	Ala				
			405					410						415					
Ala	Asp	Ile	Ser	Gly	Phe	Leu	Gly												
			420																

<210> 1037

<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> GDC

<222> (101)..(1108)

<223> RXN01027

<400> 1037

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gaactgtgtg	caccacaacg	cggaagggtga	atgcgaccca	atg	gca	aat	aag	aac		115
				Met	Ala	Asn	Lys	Asn		
					1			5		

aat	aag	cct	cat	gag	gtg	gac	aaa	gac	caa	gat	tca	gcc	atg	ctg	atc	163
Asn	Lys	Pro	His	Glu	Val	Asp	Lys	Asp	Gln	Asp	Ser	Ala	Met	Leu	Ile	
			10					15						20		

aac	ggt	cgc	ctg	caa	cag	atc	ccg	gcg	cgt	ccc	act	gag	gaa	ttc	acc	211
Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro	Thr	Glu	Glu	Phe	Thr	
			25					30						35		

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr
 40 45 50

aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat 307
 Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp
 55 60 65

gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg 355
 Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro
 70 75 80 85

aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt 403
 Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg
 90 95 100

ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc 451
 Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr
 105 110 115

aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc 499
 Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val
 120 125 130

ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca 547
 Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala
 135 140 145

tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca 595
 Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala
 150 155 160 165

gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc 643
 Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg
 170 175 180

cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag 691
 His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys
 185 190 195

cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc 739
 Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro
 200 205 210

atg ttg ttg ccc ttc aaa ccc acc gca att tac tcg gcg gtg ccc gat 787
 Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp
 215 220 225

cgc tgc caa gcc acc gcg ctc ccc ctt gcc gat gag ctc ggc ctc gac 835
 Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp
 230 235 240 245

gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc 883
 Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro
 250 255 260

gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg 931
 Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val
 265 270 275

ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg 979

Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa
 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc
 1075

Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg ttttaaggcct
 1128

Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 330 335

cca
 1131

<210> 1038

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 1038

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp
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Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro
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Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
 35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
 290 295 300

Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
 305 310 315 320

Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 325 330 335

<210> 1039

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> FRXA01024

<400> 1039

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gaactgtgtg caccacaacg cggaaggtga atcgcaccca atg gca aat aag aac 115
 Met Ala Asn Lys Asn
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr

40	45	50	
aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat			307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp			
55	60	65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg			355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro			
70	75	80	85
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt			403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg			
	90	95	100
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc			451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr			
	105	110	115
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc			499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val			
	120	125	130
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca			547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala			
	135	140	145
tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca			595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala			
	150	155	160
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc			643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg			
	170	175	180
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag			691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys			
	185	190	195
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc			739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro			
	200	205	210

atg ttg ttg ccc ttc aaa	757
Met Leu Leu Pro Phe Lys	
215	

<210> 1040

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1040

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1				5					10					15	

Ser	Ala	Met	Leu	Ile	Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro
			20					25					30		

Thr	Glu	Glu	Phe	Thr	Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp
	35						40					45			

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys
 210 215

<210> 1041
 <211> 257
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(234)
 <223> FRXA01027

<400> 1041
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 Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln
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ggc ggc gtg ccg atg atc gtt ggc cag ggc gac atc att ccg gaa atg 96
 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30

atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45

aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 65 70 75

taggagcgcg tttaaggcct cca 257

<210> 1042

<211> 78

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1042

Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln
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Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30

Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 65 70 75

<210> 1043

<211> 651

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01528

<400> 1043

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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115
 Val Asn Gln Ala Trp
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

55 60 65
 aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
 Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
 70 75 80 85
 ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
 Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
 90 95 100
 gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
 Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
 105 110 115
 gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
 Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
 120 125 130
 tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547
 Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
 135 140 145
 cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
 Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
 150 155 160 165
 aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaacccg 648
 Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
 170 175
 aac 651
 <210> 1044
 <211> 176
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1044
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 Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
 20 25 30
 Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
 35 40 45
 Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
 50 55 60
 Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
 65 70 75 80
 Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
 85 90 95
 Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
 100 105 110
 His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu

115	120	125
Val Thr Glu Val Ala Trp	Ile Pro Ala Asn Gln Leu	Ile Glu His Leu
130	135	140
Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu		
145	150	155
Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg		
165	170	175

<210> 1045
 <211> 541
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(541)
 <223> RXA00072

<400> 1045
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aagaatctct cgaaagacac aaaagaggtg agtcgcaaca atg agc ttt caa cta 115
 Met Ser Phe Gln Leu
 1 5

gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser
 10 15 20

ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys
 25 30 35

cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala
 40 45 50

agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala
 55 60 65

att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355
 Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala
 70 75 80 85

gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403
 Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr
 90 95 100

cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr
 105 110 115

tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499

Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln
 120 125 130

gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541
 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala
 135 140 145

<210> 1046

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

Met Ser Phe Gln Leu Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys
 1 5 10 15

Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser
 20 25 30

Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala
 35 40 45

Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu
 50 55 60

His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val
 65 70 75 80

Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe
 85 90 95

Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln
 100 105 110

Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu
 115 120 125

Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser
 130 135 140

Asn Pro Ala
 145

<210> 1047

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXA01878

<400> 1047

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atagtagaaa tctggcatcc aataggtaga ttgggatgct atg gaa gaa ccc tca 115
 Met Glu Glu Pro Ser
 1 5

ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag	163
Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys	
10 15 20	
ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat	211
Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp	
25 30 35	
ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac	259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn	
40 45 50	
gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc	307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala	
55 60 65	
ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt	355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg	
70 75 80 85	
ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt	403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu	
90 95 100	
gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa	451
Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln	
105 110 115	
tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac	499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr	
120 125 130	
aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc	547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr	
135 140 145	
atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg	595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu	
150 155 160 165	
gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg	643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala	
170 175 180	
tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc	691
Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val	
185 190 195	
ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc	739
Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg	
200 205 210	
gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg	787
Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp	
215 220 225	
ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct	835
Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala	
230 235 240 245	

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu
 250 255 260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val
 265 270 275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys
 280 285 290

tgaaaattac cgctaaggcg tgg
 1002

<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

Met Glu Glu Pro Ser Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg
 1 5 10 15

Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln
 20 25 30

Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala
 35 40 45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly
 50 55 60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val
 65 70 75 80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp
 85 90 95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala
 100 105 110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val
 115 120 125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met
 130 135 140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu
 145 150 155 160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val
 165 170 175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
260 265 270

Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
275 280 285

Gln Lys Asp Glu Lys
290

<210> 1049

<211> 1545

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1531)

<223> RXN02281

<400> 1049

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cctataaaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
Val Gln Lys Asp Ser
1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg
70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn
90 95 100

tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451

Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro
 105 110 115
 gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt 499
 Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly
 120 125 130
 gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac 547
 Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp
 135 140 145
 gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg 595
 Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro
 150 155 160 165
 ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc 643
 Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile
 170 175 180
 gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg 691
 Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu
 185 190 195
 ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg 739
 Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met
 200 205 210
 tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca 787
 Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro
 215 220 225
 aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa 835
 Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu
 230 235 240 245
 acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc 883
 Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile
 250 255 260
 acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca 931
 Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro
 265 270 275
 tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa 979
 Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu
 280 285 290
 gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc
 1027
 Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg
 295 300 305
 atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att
 1075
 Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
 310 315 320 325
 ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
 1123
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga

1545

Thr Leu Gly Glu Val Pro Phe Arg
470 475

<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp
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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asn Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
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Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
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<211> 1191

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1168)

<223> FRXA02281

<400> 1051

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 Val Gln Lys Asp Ser 5
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gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu 20
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att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn 35
 25 30

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr 50
 40 45

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly 65
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tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg 85
 70 75 80

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 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn

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Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro				
	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt				499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly				
	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac				547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp				
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gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg				595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro				
	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc				643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile				
	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg				691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu				
	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg				739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met				
	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca				787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro				
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aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa				835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu				
	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc				883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile				
	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro				
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Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu				
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1027				
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg				
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1075				
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile				
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ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc
1168

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1191

<210> 1052

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 1052

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35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
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<211> 1146

<212> DNA

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<222> (101)..(1123)

<223> RXN01240

<400> 1053

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 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp
 25 30 35
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 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser
 40 45 50
 agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile
 55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc	355
Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile	
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Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln	
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Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg	
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Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val	
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185 190 195	
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Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val	
215 220 225	
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Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn	
230 235 240 245	
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Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val	
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aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac	979
Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp	
280 285 290	
gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc	1027
Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val	
295 300 305	

gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa
1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac
1123

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1146

<210> 1054

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

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20 25 30

Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg
35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn
50 55 60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

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Met	Ala	Trp	Met	Arg	Gln	Leu	Leu	Asp	Trp	Gln	Lys	Glu	Ala	Ala	Asp		
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ccc	aac	gag	ttc	ctg	gac	agc	ctg	cgc	tac	gat	ctg	act	tcc	aag	cag	451	
Pro	Asn	Glu	Phe	Leu	Asp	Ser	Leu	Arg	Tyr	Asp	Leu	Thr	Ser	Lys	Gln		
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Ile	Phe	Val	Phe	Thr	Pro	Lys	Gly	Asp	Val	Val	Asn	Leu	Pro	Val	Asn		
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Ser	Thr	Pro	Val	Asp	Phe	Ala	Tyr	Ala	Val	His	Thr	Glu	Val	Gly	His		
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cgc	tgc	atc	ggc	gcc	aaa	atc	aac	ggc	aaa	ctg	gtc	gct	ttg	gaa	acg	595	
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Lys	Leu	Lys	Ser	Gly	Asp	Arg	Val	Glu	Val	Phe	Thr	Ser	Lys	Asp	Gln		
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Tyr	Leu	Glu	Ala	Gly	Arg	Asp	Ala	Leu	Ala	Ala	Val	Ile	Gln	Arg	Gly		
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Ala	Thr	Glu	Leu	His	Tyr	Pro	Asp	Val	Asp	Ala	Leu	Tyr	Thr	Ala	Ile		
				250					255					260			
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Gly	Ser	Gly	Ser	Val	Ser	Ala	Gln	His	Val	Val	Asn	Arg	Leu	Met	Ala		
			265				270						275				
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Ile	Phe	Gly	Asp	Glu	Glu	Asp	Ala	Glu	Asp	Ala	Leu	Val	Ala	Arg	Thr		
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cca	ttc	agc	gag	ctg	gtc	aac	tcc	cgt	gcc	acc	acg	gaa	agc	agc	acc	1027	
Pro	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr	Thr	Glu	Ser	Ser	Thr		
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1075

Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met Ala Lys Leu Ala Lys
310 315 320 325

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1123

Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe Gly Phe Val Thr Arg
330 335 340

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1171

Gly Gly Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Val Glu Lys
345 350 355

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1219

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<210> 1056

<211> 378

<212> PRT

<213> Corynebacterium glutamicum

<400> 1056

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35 40 45

Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala
50 55 60

Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln
65 70 75 80

Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln
85 90 95

Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp
100 105 110

Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val
115 120 125

Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His
130 135 140

Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu
145 150 155 160

Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe
165 170 175

Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe
180 185 190

Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys
195 200 205

Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala
210 215 220

Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser
225 230 235 240

Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala
245 250 255

Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val
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Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala
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305 310 315 320

Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe
325 330 335

Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys
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<212> DNA

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<222> (101)..(1036)

<223> RXN01940

<400> 1057

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Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu	
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Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly	
25 30 35	
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Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala	
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Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro	
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Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly	
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Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu	
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Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala	
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Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro
 250 255 260

ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala
 265 270 275

gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val
 280 285 290

gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag
 1027

Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys
 295 300 305

cgc atc gga tagacctgtt cacaaggttg tta
 1059

Arg Ile Gly
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<210> 1058
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1058

Met Thr Thr Lys Ile Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala
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Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly
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Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn
 35 40 45

Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg
 50 55 60

Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile
 65 70 75 80

His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro
 85 90 95

Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr
 100 105 110

Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro
 115 120 125

Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu
 130 135 140

Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn
 145 150 155 160

Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala
 165 170 175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp
 180 185 190
 Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn
 195 200 205
 Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala
 210 215 220
 Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val
 225 230 235 240
 His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr
 245 250 255
 Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr
 260 265 270
 Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr
 275 280 285
 Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val
 290 295 300
 Ile Asp Ala Val Lys Arg Ile Gly
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<210> 1059

<211> 602

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(579)

<223> FRXA01940

<400> 1059

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Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu	
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atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc	144
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe	
35 40 45	
aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag	192
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys	
50 55 60	
tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca	240
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala	
65 70 75 80	
aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc	288
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala	

	85	90	95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac				336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp				
	100	105	110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca				384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala				
	115	120	125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat				432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp				
	130	135	140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc				480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe				
	145	150	155	160
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg				528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu				
	165	170	175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc				576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile				
	180	185	190	
gga tagacctgtt cacaagggttg tta				602
Gly				

<210> 1060

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 1060

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20 25 30

Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe
35 40 45

Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys
50 55 60

Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala
65 70 75 80

Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala
85 90 95

Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp
100 105 110

Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala
115 120 125

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp
 130 135 140
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe
 145 150 155 160
 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu
 165 170 175
 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile
 180 185 190

Gly

<210> 1061
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1003)
 <223> RXA02559

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aacccaaccc caaaaccaga aaacactaag ctcgtgagac atg att cct gtt ctc 115
 Met Ile Pro Val Leu
 1 5

atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu
 10 15 20

gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr
 25 30 35

acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259
 Thr Ala Gly Asp Val Asp Val Lys Gln Thr Ala Ile Asp Thr Arg Trp
 40 45 50

gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln
 55 60 65

cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly
 70 75 80 85

gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu
 90 95 100

ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr
 105 110 115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499
 Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro
 120 125 130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547
 Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn
 135 140 145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595
 Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala
 150 155 160 165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643
 Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu
 170 175 180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691
 Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu
 185 190 195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739
 Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met
 200 205 210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787
 Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu
 215 220 225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835
 Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile
 230 235 240 245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883
 Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro
 250 255 260

ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931
 Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys
 265 270 275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979
 Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His
 280 285 290

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 295 300

<210> 1062

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 1062

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Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala
 35 40 45
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro
 50 55 60
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr
 65 70 75 80
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His
 85 90 95
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu
 100 105 110
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu
 115 120 125
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr
 130 135 140
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val
 145 150 155 160
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile
 165 170 175
 Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp
 180 185 190
 Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu
 195 200 205
 His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln
 210 215 220
 Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile
 225 230 235 240
 Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val
 245 250 255
 Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg
 260 265 270
 Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp
 275 280 285
 Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu
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<210> 1063

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1027)

<223> RXA02497

<400> 1063

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                               Val Arg Leu Gly Val
                               1           5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
                10                15                20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
                25                30                35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
                40                45                50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
                55                60                65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
                70                75                80                85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
                90                95                100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
                105                110                115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
                120                125                130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
                135                140                145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
                150                155                160                165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
                170                175                180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
                185                190                195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
                200                205                210

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cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
 215 220 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
 280 285 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag
 1027
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<210> 1064

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1064

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 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
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Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
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Asp Lys Gly Leu Glu
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<210> 1065
 <211> 2226
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 <213> Corynebacterium glutamicum

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 <222> (101)..(2203)
 <223> RXN01079

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 Met Asp Phe His Ala
 1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu	
		40					45					50				
gtt	gaa	aac	aag	tac	tat	gac	cca	atc	gtt	ctg	gac	aag	tac	gac	ttc	307
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe	
	55					60					65					
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg	
	70				75				80						85	
ttc	cag	tcc	ttc	ctc	ggg	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu	
				90				95						100		
aag	acc	ttc	gac	ggg	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val	
		105						110					115			
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu	
		120					125					130				
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro	
	135					140					145					
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys	
	150				155					160					165	
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile	
				170					175					180		
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggg	ggc	gta	gcg	ttg	ctg	691
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu	
			185					190					195			
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggg	gca	ccg	att	aag	aag	att	gaa	aac	739
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn	
		200					205						210			
cag	tct	tcc	ggg	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe	
	215					220					225					
tcc	tac	gct	aac	cag	ctg	ggg	gct	cgt	cag	ggg	gca	ggg	gct	gtg	tac	835
Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr	
	230				235					240				245		
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883
Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg	
			250					255						260		
gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggg	gtt	931
Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr	Leu	Ser	Leu	Gly	Val	
		265					270						275			
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979
Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met	

280	285	290
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1027		
Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile Tyr Gly Lys Pro Phe		
295	300	305
gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac		
1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp		
310	315	320 325
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg		
1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu		
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gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac		
1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp		
	345	350 355
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac		
1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn		
	360	365 370
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat		
1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp		
	375	380 385
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt		
1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly		
390	395	400 405
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc		
1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr		
	410	415 420
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc		
1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser		
	425	430 435
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc		
1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala		
	440	445 450
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac		
1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His		
	455	460 465
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt		
1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe		
470	475	480 485

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act
1603

Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr
490 495 500

gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc
1651

Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr
505 510 515

ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc
1699

Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser
520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc
1747

Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr
535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg
1795

Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu
550 555 560 565

ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac
1843

Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr
570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag
1891

Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu
585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac
1939

Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His
600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc
1987

Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly
615 620 625

tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac
2035

Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp
630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt
2083

Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg
650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc
2131

Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr
665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt
2179

Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val
680 685 690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatatc ccc
2226

Asp Gly Cys Val Ser Cys Met Leu
695 700

<210> 1066

<211> 701

<212> PRT

<213> Corynebacterium glutamicum

<400> 1066

Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn
1 5 10 15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe
20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
195 200 205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
210 215 220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly
225 230 235 240

1462

ggt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307
Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe
55 60 65

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cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355
Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg
  70                      75                      80                      85

ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403
Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu
                      90                      95                      100

aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451
Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val
                      105                      110                      115

tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499
Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu
                      120                      125                      130

aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547
Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro
                      135                      140                      145

acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595
Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys
150                      155                      160                      165

ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643
Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile
                      170                      175                      180

aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691
Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu
                      185                      190                      195

ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739
Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile
                      200                      205                      210

cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787
Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe
215                      220                      225

tcc 790
Ser
230

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<210> 1068
 <211> 230
 <212> PRT
 <213> *Corynebacterium glutamicum*

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<400> 1068
Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn
  1                      5                      10                      15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe
                20                      25                      30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
                35                      40                      45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

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50 55 60
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
 195 200 205
 Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
 210 215 220
 Leu Glu Asp Ala Phe Ser
 225 230

<210> 1069

<211> 1364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1341)

<223> FRXA01084

<400> 1069

tcc ttt ctg gat acc aag cgc gag aac gcc gat gag aag atc cgc atc 48
 Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile
 1 5 10 15

aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg 96
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30

gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag 144
 Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45

cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac 192
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr

50	55	60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg			240
Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala			
65	70	75	80
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac			288
Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr			
	85	90	95
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa			336
Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu			
	100	105	110
ggt cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc			384
Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser			
	115	120	125
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa			432
Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu			
	130	135	140
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat			480
Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp			
145	150	155	160
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act			528
Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr			
	165	170	175
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag			576
Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys			
	180	185	190
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac			624
Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His			
	195	200	205
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg			672
Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu			
	210	215	220
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt			720
Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg			
225	230	235	240
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc			768
Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe			
	245	250	255
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca			816
Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala			
	260	265	270
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag			864
Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys			
	275	280	285
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc			912
Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala			
	290	295	300

gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac
 1008
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc
 1056
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc
 1104
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct
 1152
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc
 1200
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca
 1248
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt
 1296
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg
 1341
 Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
 435 440 445

taaaagcact taaaaatattc ccc
 1364

<210> 1070

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile
 1 5 10 15

Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30

Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr
 50 55 60
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala
 65 70 75 80
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr
 85 90 95
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu
 100 105 110
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser
 115 120 125
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu
 130 135 140
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp
 145 150 155 160
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr
 165 170 175
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys
 180 185 190
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His
 195 200 205
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu
 210 215 220
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg
 225 230 235 240
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe
 245 250 255
~~Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala~~
~~260 265 270~~
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
 275 280 285
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
 290 295 300
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe

<400> 1071																
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cgaaaagcaa aaaaatttgt agaagggaag agcgcaccta atg gct gct gat tct																115
Met Ala Ala Asp Ser																
1 5																
gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta	163															
Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val																
10 15 20																
aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc	211															
Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val																
25 30 35																
tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta	259															
Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val																
40 45 50																
tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc	307															
Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala																
55 60 65																
gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag	355															
Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln																
70 75 80 85																
ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac	403															
Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His																
90 95 100																
gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca	451															
Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala																

105	110	115	
aag agt tac tcc aac atc ttc atg act ctg gcc tcc acc gcg gaa atc			499
Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala Ser Thr Ala Glu Ile			
120	125	130	
aac gat gcg ttc cgt tgg tct gag gaa aat gaa aac ctg cag cgc aag			547
Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu Asn Leu Gln Arg Lys			
135	140	145	
gca aag atc atc ctg tct tac tat gag ggc gat gat cca cta aag cgc			595
Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp Asp Pro Leu Lys Arg			
150	155	160	165
aag atc gcc tcc gtg atc ctg gag tcc ttc ctg ttc tac tcc ggc ttc			643
Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu Phe Tyr Ser Gly Phe			
170	175	180	
tac ctc cca atg tat tgg tcc agc cac tcc aag ctg gcc aac acc gcc			691
Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys Leu Ala Asn Thr Ala			
185	190	195	
gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac tac			739
Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr Tyr			
200	205	210	
att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag cgt			787
Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu Arg			
215	220	225	
cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt tac			835
Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu Tyr			
230	235	240	245
gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga tgg			883
Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly Trp			
250	255	260	
acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc ctc			931
Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala Leu			
265	270	275	
aac aac ctt ggc tac gaa gga ttc ttc cca gcg gat gaa acc aag gtc			979
Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys Val			
280	285	290	
tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac cac			1027
Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn His			
295	300	305	
gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca gaa			1075
Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala Glu			
310	315	320	325
aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag			1122
Asn Thr Glu Asp Asp Asp Trp Asp Phe			
330			

cgc
1125

<210> 1072

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 1072

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His Val Ala Pro Val Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser
20 25 30

Lys Asp Leu Glu Val Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro
35 40 45

Glu Lys Val Pro Val Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn
50 55 60

Glu Val Glu Lys Ala Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu
65 70 75 80

Leu Asp Thr Ile Gln Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp
85 90 95

Ala Asp Ser Leu His Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met
100 105 110

Glu Ser Val His Ala Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala
115 120 125

Ser Thr Ala Glu Ile Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu
130 135 140

Asn Leu Gln Arg Lys Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp
145 150 155 160

Asp Pro Leu Lys Arg Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu
165 170 175

Phe Tyr Ser Gly Phe Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys
180 185 190

Leu Ala Asn Thr Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala
195 200 205

Val His Gly Tyr Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys
210 215 220

Glu Thr Pro Glu Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu
225 230 235 240

Leu Tyr Asp Leu Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr
245 250 255

Asp Asp Leu Gly Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn
260 265 270

Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala
275 280 285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn
290 295 300

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val
305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
325 330

<210> 1073

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01920

<400> 1073

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tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag 96
Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
20 25 30

cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt 144
Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
35 40 45

tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga 192
Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
50 55 60

tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc 240
Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
65 70 75 80

ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag 288
Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
85 90 95

gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac 336
Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
100 105 110

cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca 384
His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
115 120 125

gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag 434
Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
130 135

cgc 437

<210> 1074

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 1074

Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
 1 5 10 15

Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
 20 25 30

Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
 35 40 45

Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
 50 55 60

Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
 65 70 75 80

Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
 85 90 95

Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
 100 105 110

His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
 115 120 125

Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 130 135

<210> 1075

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA01080

<400> 1075

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ttgcgcacaa acggtatttta gaagggaagt gagttcgagg atg cta atc gtg tat 115
 Met Leu Ile Val Tyr
 1 5

ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163
 Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp
 10 15 20

tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211
 Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys
 25 30 35

atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259
 Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val
 40 45 50

tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307
 Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg
 55 60 65

ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355
 Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala
 70 75 80 85

ggt gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403
 Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile
 90 95 100

att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451
 Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met
 105 110 115

ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499
 Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn
 120 125 130

gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544
 Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg
 135 140 145

taaaccttaa aacttaatca atc 567

<210> 1076

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 1076

Met Leu Ile Val Tyr Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe
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Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val
 20 25 30

Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr
 35 40 45

Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro
 50 55 60

Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile
 65 70 75 80

Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly
 85 90 95

Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr
 100 105 110

Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly
 115 120 125

Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro
 130 135 140

Val Thr Ser Arg
 145

<210> 1077

<211> 650

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

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Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr	
1 5 10 15	
gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc	96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu	
20 25 30	
tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac	144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn	
35 40 45	
acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct	192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala	
50 55 60	
cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg	240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu	
65 70 75 80	
atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc	288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly	
85 90 95	
gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct	336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala	
100 105 110	
gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg	384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala	
115 120 125	
aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc	432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val	
130 135 140	
aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac	480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp	
145 150 155 160	
ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag	528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys	
165 170 175	

gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

gac taattagttc tggctagatc ggg 650
 Asp

<210> 1078
 <211> 209
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1078
 Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr
 1 5 10 15

Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
 20 25 30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

Asp

<210> 1079
 <211> 630
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(630)
 <223> RXA01416

<400> 1079
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 Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro
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 gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca 96
 Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
 20 25 30
 ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt 144
 Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45
 gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag 192
 Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60
 gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg 240
 Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80
 ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac 288
 Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95
 atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac 336
 Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110
 agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct 384
 Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125
 gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc 432
 Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140
 atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt 480
 Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160
 gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag 528
 Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175
 acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag 576
 Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

tac aac 630
 Tyr Asn
 210

<210> 1080

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1080

Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro
 1 5 10 15

Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
 20 25 30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140

Ile Asn Gly Arg Gly Val Thr Asn Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

Tyr Asn
 210

<210> 1081

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXA01486

<400> 1081

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atcgccgagc	agaactaaac	atgaggagac	ctactcgcat	atg	agc	gat	gta	aag	115
				Met	Ser	Asp	Val	Lys	
				1				5	

gac	ttc	gaa	gac	acc	gaa	ttt	ggc	ctg	atc	gag	gcc	gtc	gca	acc	atc	163
Asp	Phe	Glu	Asp	Thr	Glu	Phe	Gly	Leu	Ile	Glu	Ala	Val	Ala	Thr	Ile	
				10				15						20		

gac	aac	ggc	gac	ttc	gga	acc	cgc	acc	atc	cgt	ttt	gaa	acc	ggc	caa	211
Asp	Asn	Gly	Asp	Phe	Gly	Thr	Arg	Thr	Ile	Arg	Phe	Glu	Thr	Gly	Gln	
				25				30						35		

ctt	gcc	cgc	cag	gca	gat	ggc	gca	gtg	acc	acc	tac	ctc	gac	gat	gac	259
Leu	Ala	Arg	Gln	Ala	Asp	Gly	Ala	Val	Thr	Thr	Tyr	Leu	Asp	Asp	Asp	
				40				45						50		

acg	atg	ctg	ctg	gca	acc	acc	acc	gca	tcc	aac	cag	cca	cgc	gag	ggc	307
Thr	Met	Leu	Leu	Ala	Thr	Thr	Thr	Ala	Ser	Asn	Gln	Pro	Arg	Glu	Gly	
				55				60						65		

ttt	gac	ttc	ttc	cca	ctg	acc	gtg	gac	gtt	gaa	gag	cgt	atg	tac	gca	355
Phe	Asp	Phe	Phe	Pro	Leu	Thr	Val	Asp	Val	Glu	Glu	Arg	Met	Tyr	Ala	
				70				75					80		85	

gct	ggc	cgc	atc	cct	ggc	tct	ttc	ttc	cgt	cgg	gag	ggc	cgc	cca	tcc	403
Ala	Gly	Arg	Ile	Pro	Gly	Ser	Phe	Phe	Arg	Arg	Glu	Gly	Arg	Pro	Ser	
				90						95				100		

acc	gaa	gct	atc	ctg	gct	tgc	cgt	ctc	atc	gac	cgc	cca	ctg	cgc	cca	451
Thr	Glu	Ala	Ile	Leu	Ala	Cys	Arg	Leu	Ile	Asp	Arg	Pro	Leu	Arg	Pro	
				105				110						115		

acc	ttt	gtt	aag	ggc	ctg	cgc	aat	gag	gtt	cag	atc	gtt	gtc	acc	gtc	499
Thr	Phe	Val	Lys	Gly	Leu	Arg	Asn	Glu	Val	Gln	Ile	Val	Val	Thr	Val	
				120				125					130			

atg	tcc	atg	aac	cct	gag	gat	tac	tac	gat	gtc	gta	gca	atc	aac	gga	547
Met	Ser	Met	Asn	Pro	Glu	Asp	Tyr	Tyr	Asp	Val	Val	Ala	Ile	Asn	Gly	
				135					140					145		

gct	tcc	gca	gca	acc	cgc	atc	tcc	gga	ctt	cct	gtc	tcc	ggc	gct	gtc	595
Ala	Ser	Ala	Ala	Thr	Arg	Ile	Ser	Gly	Leu	Pro	Val	Ser	Gly	Ala	Val	
				150				155						160	165	

ggc	ggc	gtt	cgc	atg	gca	ctg	gtt	ggc	gat	gaa	aag	cac	cca	gaa	ggc	643
Gly	Gly	Val	Arg	Met	Ala	Leu	Val	Gly	Asp	Glu	Lys	His	Pro	Glu	Gly	
				170					175					180		

caa	tgg	gtt	gca	ttc	cca	acc	cac	gct	caa	cat	gag	cag	tcc	gta	ttt	691
Gln	Trp	Val	Ala	Phe	Pro	Thr	His	Ala	Gln	His	Glu	Gln	Ser	Val	Phe	
				185				190						195		

gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739
 Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys
 200 205 210

acc ttc tcc gac gtc gca 757
 Thr Phe Ser Asp Val Ala
 215

<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

Met Ser Asp Val Lys Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu
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Ala Val Ala Thr Ile Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg
 20 25 30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr
 35 40 45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn
 50 55 60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu
 65 70 75 80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg
 85 90 95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp
 100 105 110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln
 115 120 125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val
 130 135 140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro
 145 150 155 160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu
 165 170 175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His
 180 185 190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg
 195 200 205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala
 210 215

<210> 1083

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01678

<400> 1083

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cggctatatc	tctgcaactg	cagctcacc	cggtgcagca	atg	ctg	aaa	tgt	gca	115
				Met	Leu	Lys	Cys	Ala	
				1				5	

gtc	gat	gaa	gcc	gct	ggc	gga	cgc	gcc	caa	gct	ttc	gta	tcc	tca	ggc	163
Val	Asp	Glu	Ala	Ala	Gly	Gly	Arg	Ala	Gln	Ala	Phe	Val	Ser	Ser	Gly	
				10				15							20	

gat	aac	att	ggt	ggc	agc	ccg	ttc	caa	tcc	tcc	att	ctt	ggt	gat	gaa	211
Asp	Asn	Ile	Gly	Gly	Ser	Pro	Phe	Gln	Ser	Ser	Ile	Leu	Gly	Asp	Glu	
			25					30					35			

ccc	acc	ttg	gaa	gca	ctc	aac	caa	atg	ggt	ctt	gat	tac	tca	gca	gtg	259
Pro	Thr	Leu	Glu	Ala	Leu	Asn	Gln	Met	Gly	Leu	Asp	Tyr	Ser	Ala	Val	
		40					45					50				

ggc	aac	cac	gaa	ttt	gat	aaa	ggc	tac	gca	gac	tta	agc	agt	cga	gtc	307
Gly	Asn	His	Glu	Phe	Asp	Lys	Gly	Tyr	Ala	Asp	Leu	Ser	Ser	Arg	Val	
	55					60					65					

gct	gac	ctt	gct	gat	ttt	gat	tat	ctc	ggc	gca	aac	gtt	gag	ggc	gaa	355
Ala	Asp	Leu	Ala	Asp	Phe	Asp	Tyr	Leu	Gly	Ala	Asn	Val	Glu	Gly	Glu	
70					75				80						85	

aac	cca	gat	ctt	gca	cca	tat	gga	att	tct	cac	ctt	gat	ggt	gtg	aag	403
Asn	Pro	Asp	Leu	Ala	Pro	Tyr	Gly	Ile	Ser	His	Leu	Asp	Gly	Val	Lys	
			90					95					100			

gtt	gct	ttc	gta	ggc	acc	gta	tcc	caa	gaa	act	ccg	atg	ttg	gtc	aat	451
Val	Ala	Phe	Val	Gly	Thr	Val	Ser	Gln	Glu	Thr	Pro	Met	Leu	Val	Asn	
			105					110					115			

tct	gaa	ggc	att	gag	gga	atc	acg	ttt	act	gac	cca	ctt	gaa	gca	acc	499
Ser	Glu	Gly	Ile	Glu	Gly	Ile	Thr	Phe	Thr	Asp	Pro	Leu	Glu	Ala	Thr	
	120					125						130				

aac	cgt	gta	gct	gat	gaa	ctc	gtg	gga	agt	ggc	gca	gca	gat	gtt	gtc	547
Asn	Arg	Val	Ala	Asp	Glu	Leu	Val	Gly	Ser	Gly	Ala	Ala	Asp	Val	Val	
	135					140					145					

gtt	gcg	ctt	tac	cac	gaa	ggc	att	acc	ggc	acc	gaa	gca	tggt	tca	gaa	595
Val	Ala	Leu	Tyr	His	Glu	Gly	Ile	Thr	Gly	Thr	Glu	Ala	Trp	Ser	Glu	
150					155				160						165	

aat	atc	gac	gtt	gtt	ttc	gca	ggt	cac	acc	cac	taagttcgtg	atctaggaac	648
Asn	Ile	Asp	Val	Val	Phe	Ala	Gly	His	Thr	His			
			170					175					

cga													651
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<210> 1084

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1084

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Phe Val Ser Ser Gly Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser
 20 25 30

Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu
 35 40 45

Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp
 50 55 60

Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala
 65 70 75 80

Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His
 85 90 95

Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr
 100 105 110

Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp
 115 120 125

Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly
 130 135 140

Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr
 145 150 155 160

Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His
 165 170 175

<210> 1085

<211> 1359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXA01679

<400> 1085

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ctaagttcgt gatctaggaa ccgacaacgg tccactaate atg cag tct gga aac 115
 Met Gln Ser Gly Asn
 1 5

tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc	163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
10 15 20	
ggt gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tac gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
200 205 210	
gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly
 250 255 260

caa gcc cag att tcc atc acc cca tcc ggt gag ttc aat gcg ggt gaa 931
 Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu
 265 270 275

acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr
 280 285 290

gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca
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 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro
 295 300 305

att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg
 1075
 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala
 310 315 320 325

aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc
 1123
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu
 330 335 340

gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att
 1171
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile
 345 350 355

gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta
 1219
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu
 360 365 370

gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta
 1267
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu
 375 380 385

gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag
 1315

Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln
 390 395 400 405

atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat
 1359
 Ile Gln Gln Gln Ile Phe Ala
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<210> 1086
 <211> 412
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1086
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Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu
 20 25 30
 Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala
 35 40 45
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu
 50 55 60
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly
 65 70 75 80
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met
 85 90 95
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr
 100 105 110
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe
 115 120 125
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser
 130 135 140
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala
 145 150 155 160
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu
 165 170 175
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile
 180 185 190
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro
 195 200 205
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn
 210 215 220
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly
 225 230 235 240
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val
 245 250 255
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu
 260 265 270
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr
 275 280 285
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu
 290 295 300
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly
 305 310 315 320
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser
 325 330 335
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser

340	345	350
Met Pro Val Glu Ile Val Gly	Ala Glu Gln Pro Ala	Pro Gln Pro Ala
355	360	365
Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly	Leu Leu Gly Ile	
370	375	380
Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro		
385	390	395
Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala		
405	410	

<210> 1087

<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1048)

<223> RXN01488

<400> 1087

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gccccgacctt aaaaataaaa acctgaaagg ttaaaaacgc	atg agc aaa aaa gcc	115
	Met Ser Lys Lys Ala	
	1 5	

atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac	163
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr	
10 15 20	

gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac	211
Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr	
25 30 35	

ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt	259
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu	
40 45 50	

gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac	307
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His	
55 60 65	

gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att	355
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile	
70 75 80 85	

cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca	403
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser	
90 95 100	

aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc	451
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr	
105 110 115	

cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg	499
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His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu
    120                      125                      130

tct gcg gca atc gca aag gat cca agc ttt gct tcc aag gct cac gtg 547
Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val
    135                      140                      145

gtc atc atg ggt ggc gcc ttg act gtc cca ggc aac gtc agc aca tgg 595
Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp
    150                      155                      160                      165

gca gaa gca aac atc aac cag gac cca gat gca gca aac gat ctg ttc 643
Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe
    170                      175                      180

cgt tcc ggt gca gat gtc acc atg atc ggt ctt gat gtc acc ctg cag 691
Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln
    185                      190                      195

acc ctt ctt acc aag aag cac act gcg cag tgg cgc gaa ctg ggc act 739
Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr
    200                      205                      210

cca gct gct atc gca ctg gcc gac atg act gat tac tac atc aag gca 787
Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala
    215                      220                      225

tat gag acc acc gca cca cac ctg ggc ggt tgc ggc ctg cac gac cca 835
Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro
    230                      235                      240                      245

ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act ttg ctc ccc 883
Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro
    250                      255                      260

atc aac ctc aag gta gac att gag ggc gag acc cgt gga cgc acc att 931
Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile
    265                      270                      275

ggc gat gaa gtc cgc ctc aac gat cca gtg cgc acc tcc cgc gca gct 979
Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala
    280                      285                      290

gtc gcc gta gac gtg gat cgt ttc ctt tct gaa ttc atg acc cgc atc
1027
Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile
    295                      300                      305

ggc cga gtc gca gca cag cag taaaagcagc tctggtgaag gtt
1071
Gly Arg Val Ala Ala Gln Gln
    310                      315

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<210> 1088

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 1088

Met Ser Lys Lys Ala Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala

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Leu Ala Leu Ala Tyr Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly	20	25	30
Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn	35	40	45
Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr	50	55	60
Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu	65	70	75
Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu	85	90	95
Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile	100	105	110
Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly	115	120	125
Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala	130	135	140
Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly	145	150	155
Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala	165	170	175
Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu	180	185	190
Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp	195	200	205
Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp	210	215	220
Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys	225	230	235
Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu	245	250	255
Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr	260	265	270
Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg	275	280	285
Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu	290	295	300
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<210> 1090
<211> 81
<212> PRT
<213> Corynebacterium glutamicum
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Pro Gln Gly Gln Ala Val His Arg Ala Leu Gly Arg Ile Gly Val Ser
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Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
      35              40              45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
      50              55              60

Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
  65              70              75              80

Lys

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<210> 1091
 <211> 498
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(475)
 <223> RXC00560

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 Met Arg Ile Asp Pro
 1 5
 ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
 Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
 10 15 20
 gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
 Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
 25 30 35
 cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
 Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
 40 45 50
 gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
 Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
 55 60 65
 aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag 355
 Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
 70 75 80 85
 acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt 403
 Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
 90 95 100
 gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg 451
 Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
 105 110 115
 gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt 498
 Asp Trp Leu Pro Val Val Lys Leu
 120 125

<210> 1092
 <211> 125
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1092
 Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
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Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
 20 25 30
 Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
 35 40 45
 Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
 50 55 60
 Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
 65 70 75 80
 Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
 85 90 95
 Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
 100 105 110
 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
 115 120 125

<210> 1093
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1282)
 <223> RXC01088

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 gtgaaccgaa ttttttaact gatttgaaga agcgagaata atg gga ctg tgg atc 115
 Met Gly Leu Trp Ile
 1 5

 gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
 10 15 20

 gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
 25 30 35

 atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
 40 45 50

 caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
 55 60 65

 cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355
 His Arg His Leu Ser Thr Ile Lys Glu Leu Val Asn Ala Asp Ile
 70 75 80 85

 cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403

Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala
90 95 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe
105 110 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys
120 125 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile
135 140 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val
150 155 160 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc 643
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr
170 175 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca 691
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro
185 190 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc 739
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe
200 205 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat 787
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp
215 220 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct 835
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser
230 235 240 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt 883
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val
250 255 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt 931
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe
265 270 275

gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag 979
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys
280 285 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg
1027
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val
295 300 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc
1075
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile
310 315 320 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa
1123

Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln
330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat
1171

Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp
345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca
1219

Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala
360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg
1267

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1305

Gln Gly Thr Thr Glu
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<210> 1094

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1094

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Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu
35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
50 55 60

His Glu His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
 165 170 175
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
 180 185 190
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
 195 200 205
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
 210 215 220
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
 225 230 235 240
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
 245 250 255
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
 260 265 270
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro
 275 280 285
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val
 290 295 300
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr
 305 310 315 320
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp
 325 330 335
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys
 340 345 350
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu
 355 360 365
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 370 375 380

Val Ala Arg Ile Pro Gln Gly Thr Thr Glu
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<210> 1095
 <211> 1419
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1396)
 <223> RXC02624

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											1					5
ggc	gtg	gcg	gtg	ctt	ttg	gtt	att	att	ctc	gcc	gta	gcc	tcc	cta	atg	163
Gly	Val	Ala	Val	Leu	Leu	Val	Ile	Ile	Leu	Ala	Val	Ala	Ser	Leu	Met	
				10					15					20		
ttc	acc	aat	tct	tca	atg	gtg	aat	ctt	tcg	gca	acg	att	gca	cag	ctg	211
Phe	Thr	Asn	Ser	Ser	Met	Val	Asn	Leu	Ser	Ala	Thr	Ile	Ala	Gln	Leu	
			25					30					35			
tgg	ctt	tcc	cta	aat	ctc	ggt	gcg	gtg	gac	ggc	agt	ggg	gaa	gtg	atc	259
Trp	Leu	Ser	Leu	Asn	Leu	Gly	Ala	Val	Asp	Gly	Ser	Gly	Glu	Val	Ile	
		40					45					50				
tca	gta	ctg	ccc	acg	ctt	ccc	ggc	ttt	ata	ttc	ctc	tgg	gcc	atc	gcc	307
Ser	Val	Leu	Pro	Thr	Leu	Pro	Gly	Phe	Ile	Phe	Leu	Trp	Ala	Ile	Ala	
	55					60					65					
gcg	cgc	atc	cac	cgc	gca	gtc	aaa	gat	cgt	gtc	agc	atc	gcc	gac	tta	355
Ala	Arg	Ile	His	Arg	Ala	Val	Lys	Asp	Arg	Val	Ser	Ile	Ala	Asp	Leu	
	70				75					80					85	
ggc	gtc	ctc	gca	gca	ctc	gtc	ctc	ggc	atc	ccg	ctt	gcg	ctc	acc	gcc	403
Gly	Val	Leu	Ala	Ala	Leu	Val	Leu	Gly	Ile	Pro	Leu	Ala	Leu	Thr	Ala	
				90					95					100		
atc	gca	gcg	ttc	atg	ctt	ttc	gac	gcc	tcc	agc	gtc	ctc	aac	gtc	gag	451
Ile	Ala	Ala	Phe	Met	Leu	Phe	Asp	Ala	Ser	Ser	Val	Leu	Asn	Val	Glu	
			105					110					115			
gtc	ccg	cca	atc	acg	cgc	ctc	cta	cgc	gtg	atg	ttg	ttc	cac	ctc	agc	499
Val	Pro	Pro	Ile	Thr	Arg	Leu	Leu	Arg	Val	Met	Leu	Phe	His	Leu	Ser	
		120						125					130			
gcc	ctc	ttc	ctc	ggc	atg	ggg	cca	cgc	ctg	tgg	cag	gcg	ttg	gcg	cgc	547
Ala	Leu	Phe	Leu	Gly	Met	Gly	Pro	Arg	Leu	Trp	Gln	Ala	Leu	Ala	Arg	
		135					140				145					
cgc	tac	ggt	gct	cca	gaa	tgg	ctt	atc	gac	gcc	atc	acc	caa	gct	ttc	595
Arg	Tyr	Gly	Ala	Pro	Glu	Trp	Leu	Ile	Asp	Ala	Ile	Thr	Gln	Ala	Phe	
	150				155					160					165	
cgc	ttc	ctc	atc	gca	ttt	gga	aca	gtc	tcc	ttg	gtt	tcc	gtg	ctc	gtg	643
Arg	Phe	Leu	Ile	Ala	Phe	Gly	Thr	Val	Ser	Leu	Val	Ser	Val	Leu	Val	
				170					175					180		
atg	acc	gcg	atc	aac	cac	agt	gca	ttc	acc	gcg	acc	atg	cag	ggt	tac	691
Met	Thr	Ala	Ile	Asn	His	Ser	Ala	Phe	Thr	Ala	Thr	Met	Gln	Gly	Tyr	
			185					190					195			
gac	gac	tcc	gcc	tct	gtt	gtg	gcc	ttg	atc	gtc	ctg	agc	att	ctg	tat	739
Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr	
		200					205					210				
ctg	ccc	aac	atg	atg	atc	ttt	gcg	atg	ggc	aat	ctg	atc	ggc	tca	ccc	787
Leu	Pro	Asn	Met	Met	Ile	Phe	Ala	Met	Gly	Asn	Leu	Ile	Gly	Ser	Pro	
		215					220				225					
ctt	tac	ttc	ggt	gac	gcc	tcc	atc	agc	gtc	ttc	agc	gtg	cat	tcc	gtt	835
Leu	Tyr	Phe	Gly	Asp	Ala	Ser	Ile	Ser	Val	Phe	Ser	Val	His	Ser	Val	

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro	Leu Pro Ile Leu	Ala Ala Leu Pro	Ser Glu Ala Leu	
	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp				
	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala				
	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
1027				
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly				
	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
1075				
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val				
	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
1123				
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly				
	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
1171				
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val				
	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
1219				
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu				
	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
1267				
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly				
	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
1315				
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro				
	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
1363				
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu				
	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
1416				
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg				
	425	430		
ctg				
1419				

<210> 1096

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
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Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val
 275 280 285

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala
 290 295 300
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn
 305 310 315 320
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly
 325 330 335
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys
 340 345 350
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu
 355 360 365
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu
 370 375 380
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp
 385 390 395 400
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr
 405 410 415
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
 420 425 430

<210> 1097

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> RXC02665

<400> 1097

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 atcaccgacg aagccgaacc cacaatatatt gaggtaccag gtg act aac cca atc 115
 Val Thr Asn Pro Ile
 1 5
 atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly
 10 15 20
 aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys
 25 30 35
 gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala
 40 45 50

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ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307
Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
    55                60                65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355
Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
    70                75                80                85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403
Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
    90                95                100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451
Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu
    105                110                115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499
Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
    120                125                130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547
Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
    135                140                145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600
Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
    150                155                160

ggc 603

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<210> 1098

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 1098

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Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
    1                5                10                15

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Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
    20                25                30

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```

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
    35                40                45

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Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
    50                55                60

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```

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
    65                70                75                80

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Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
    85                90                95

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Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
    100                105                110

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Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
    115                120                125

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Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly
130 135 140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
145 150 155 160

<210> 1099

<211> 1689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1666)

<223> RXC02770

<400> 1099

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ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg 115
Met Leu Val Ala Ala
1 5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
10 15 20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
25 30 35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
40 45 50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
55 60 65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
70 75 80 85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
90 95 100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
105 110 115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
120 125 130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

135	140	145	
gaa gac ctc ggt gag	cgt tgg cgt tat ctt	ttt gag cag ggc gat ttg	595
Glu Asp Leu Gly Glu	Arg Trp Arg Tyr Leu	Phe Glu Gln Gly Asp Leu	
150	155	160 165	
ttg cca gcc cat gcc	gtt gct tcc aaa gca	ggt atg acc ttg gag gag	643
Leu Pro Ala His Ala	Val Ala Ser Lys Ala	Gly Met Thr Leu Glu Glu	
	170	175 180	
ctt aat cag gcg ttg	aag gat aag gat cct	gaa gcg ttg act gaa cct	691
Leu Asn Gln Ala Leu	Lys Asp Lys Asp Pro	Glu Ala Leu Thr Glu Pro	
	185 190	195	
gct cgt gtg tgg agc	gaa ggt ttc cag ctg	tcc cag ttt gat cca gag	739
Ala Arg Val Trp Ser	Glu Gly Phe Gln Leu	Ser Gln Phe Asp Pro Glu	
	200 205	210	
ctg cag acg gct ttt	ggc ccg tac aag gtg	gat tct gtg ggt gaa ttc	787
Leu Gln Thr Ala Phe	Gly Pro Tyr Lys Val	Asp Ser Val Gly Glu Phe	
	215 220	225	
ggc gaa gtc aag ctg	gta cgc aat gag ttt	tac agt ggc gac cag gcg	835
Gly Glu Val Lys Leu	Val Arg Asn Glu Phe	Tyr Ser Gly Asp Gln Ala	
230	235	240 245	
gtt gaa gca gaa atc	acg atg tgg cct aaa	ggc tcg gat ctc agc gcc	883
Val Glu Ala Glu Ile	Thr Met Trp Pro Lys	Gly Ser Asp Leu Ser Ala	
	250	255 260	
att gcg gat aat gga	aac ctt cag atc gca	cat gtt gtg gcg tgg gag	931
Ile Ala Asp Asn Gly	Asn Leu Gln Ile Ala	His Val Val Ala Trp Glu	
	265	270 275	
agc gag ccg tgg gta	aat cgc gat gac cca	ttg aat cct tat gac att	979
Ser Glu Pro Trp Val	Asn Arg Asp Asp Pro	Leu Asn Pro Tyr Asp Ile	
	280 285	290	
aag gaa gag gtc ggt	gtt ttg act gag cag	ctc acc ttg gcc agt gcc	
1027			
Lys Glu Glu Val Gly	Val Leu Thr Glu Gln	Leu Thr Leu Ala Ser Ala	
	295	300 305	
ggt gtg ttt tac gct	gcg gag gcc cgg cag	gcg ttt gcg gcc tgc gtt	
1075			
Gly Val Phe Tyr Ala	Ala Glu Ala Arg Gln	Ala Phe Ala Ala Cys Val	
310	315	320 325	
gac cag gaa gcg gtg	gct gcg gcg tcg tca	agc atc tct gga atc gat	
1123			
Asp Gln Glu Ala Val	Ala Ala Ala Ser Ser	Ser Ile Ser Gly Ile Asp	
	330	335 340	
gtg cct gcc gta ggt	gtg cac tcg gtg cgt	cac caa aat ccg gtc gtg	
1171			
Val Pro Ala Val Gly	Val His Ser Val Arg	His Gln Asn Pro Val Val	
	345	350 355	
cac caa atc ggt gat	ctg cca gca cag cac	atg gcg gtg gat att aat	
1219			
His Gln Ile Gly Asp	Leu Pro Ala Gln His	Met Ala Val Asp Ile Asn	

360 365 370
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga
 1267
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly
 375 380 385
 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt
 1315
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys
 390 395 400 405
 gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt
 1363
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser
 410 415 420
 ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag
 1411
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln
 425 430 435
 tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat
 1459
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His
 440 445 450
 cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg
 1507
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr
 455 460 465
 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta
 1555
 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu
 470 475 480 485
 gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt
 1603
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val
 490 495 500
~~gtt gtc aat aca gaa cta gaa ggt atc gga tgg aac atg gaa cgt tgg~~
 1651
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp
 505 510 515
 tcc aga agt gag gaa taagtagtga gcgaacaagc tct
 1689
 Ser Arg Ser Glu Glu
 520

 <210> 1100
 <211> 522
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1100
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Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser
 20 25 30
 Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp
 35 40 45
 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
 50 55 60
 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
 65 70 75 80
 Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
 85 90 95
 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
 100 105 110
 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
 115 120 125
 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
 130 135 140
 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
 145 150 155 160
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
 165 170 175
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
 180 185 190
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
 195 200 205
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
 210 215 220
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
 225 230 235 240
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
 245 250 255
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
 260 265 270
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
 275 280 285
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
 290 295 300
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
 305 310 315 320
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
 325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
 340 345 350
 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
 355 360 365
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
 370 375 380
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
 385 390 395 400
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
 405 410 415
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
 420 425 430
 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
 435 440 445
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
 450 455 460
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
 485 490 495
 Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
 500 505 510
 Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
 515 520

<210> 1101
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC02238

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 Val Thr Asn Val Ser
 1 5
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95

cac 408

<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
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Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
 20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 85 90 95

<210> 1103

<211> 1298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1275)

<223> RXC01946

<400> 1103

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 Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly
 1 5 10 15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96

Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu		
			20					25					30				
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144	
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln		
		35					40					45					
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192	
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly		
		50				55					60						
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240	
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His		
65					70				75						80		
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288	
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His		
				85				90						95			
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336	
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala		
			100					105					110				
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384	
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp		
		115					120					125					
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432	
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp		
	130					135					140						
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480	
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly		
145					150					155					160		
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528	
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala		
				165				170						175			
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576	
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn		
			180					185					190				
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624	
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro		
		195					200					205					
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672	
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr		
	210					215					220						
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720	
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile		
225					230					235					240		
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggg	gca	ggg	aaa	768	
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys		
				245				250						255			
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggg	gtg	gaa	cgc	acc	gac	ggc	gaa	816	
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu		

260	265	270	
ggc ggc atc gtc acc gga tac	ggc ctc aaa atc ggc tac	ttc gcc cag	864
Gly Gly Ile Val Thr Gly Tyr	Gly Leu Lys Ile Gly Tyr	Phe Ala Gln	
275	280	285	
gaa cac gac acc atc gac ccc	gac aaa tcc gtc tgg caa aac acc atc		912
Glu His Asp Thr Ile Asp	Pro Asp Lys Ser Val Trp Gln Asn Thr Ile		
290	295	300	
gaa gcc tgc gcc gac gcc gac	caa caa agc ctc cgc agc ctc ctc gga		960
Glu Ala Cys Ala Asp Ala Asp	Gln Gln Ser Leu Arg Ser Leu Leu Gly		
305	310	315	320
tcc ttc atg ttc tcc ggc gaa	caa ctc gac caa cca gca gga aca ctc		
1008			
Ser Phe Met Phe Ser Gly Glu	Gln Leu Asp Gln Pro Ala Gly Thr Leu		
325	330	335	
tcc ggc ggt gaa aaa acc cgc	ctc gca ctg gcc acc ctc gtg tcc tcc		
1056			
Ser Gly Gly Glu Lys Thr Arg	Leu Ala Leu Ala Thr Leu Val Ser Ser		
340	345	350	
cgc gca aac gtc ctg ctt ctc	gac gag ccc acc aac aac ctt gac ccg		
1104			
Arg Ala Asn Val Leu Leu Leu	Asp Glu Pro Thr Asn Asn Leu Asp Pro		
355	360	365	
atc tcc cgc gaa cag gtc ctc	gac gca ctg cgc acc tac acc ggc gca		
1152			
Ile Ser Arg Glu Gln Val Leu	Asp Ala Leu Arg Thr Tyr Thr Gly Ala		
370	375	380	
gtc gtc ctg gtt acc cac gac	ccg ggt gca gtc aag gcc ctt gag cca		
1200			
Val Val Leu Val Thr His Asp	Pro Gly Ala Val Lys Ala Leu Glu Pro		
385	390	395	400
gaa cgc gtc atc gtg ctt cct	gat ggc acc gag gat ctt tgg aat gat		
1248			
Glu Arg Val Ile Val Leu Pro	Asp Gly Thr Glu Asp Leu Trp Asn Asp		
405	410	415	
cag tac atg gaa atc gtg gaa	ttg gcg taggttctaa ggctgtttat		
1295			
Gln Tyr Met Glu Ile Val Glu	Leu Ala		
420	425		
gct			
1298			

<210> 1104

<211> 425

<212> PRT

<213> Corynebacterium glutamicum

<400> 1104

Ile	Arg	Lys	Tyr	Ser	Arg	Leu	Glu	Glu	Gln	Phe	Gln	Ser	Leu	Gly	Gly
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Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu
 20 25 30
 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
 35 40 45
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
 50 55 60
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
 65 70 75 80
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
 85 90 95
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
 100 105 110
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
 115 120 125
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
 130 135 140
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
 145 150 155 160
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
 165 170 175
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
 180 185 190
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
 195 200 205
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
 210 215 220
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
 225 230 235 240
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys
 245 250 255
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
 260 265 270
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
 275 280 285
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
 290 295 300
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly
 305 310 315 320
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
 340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
 355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
 370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
 385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp
 405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala
 420 425

<210> 1105
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXN03171

<400> 1105
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cggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115
 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165

gac gca ttg gcg gaa tct 613
 Asp Ala Leu Ala Glu Ser
 170

<210> 1106

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
 1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
 165 170

<210> 1107

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> FRXA02857

<400> 1107

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cggctcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115
 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt gcc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165

gac gca ttg gcg gaa tct 613
 Asp Ala Leu Ala Glu Ser
 170

<210> 1108

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1108

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
 1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
 165 170

<210> 1109

<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> RXN00450

<400> 1109

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Ala Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga cgc atc 424
 Gly Ala Arg Ile Gly Arg Ile
 105

<210> 1110

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1110

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
 100 105

<210> 1111

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1111

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gttttgataa tgatctggct cgggtgggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggg gct cga atc gga 418
 Gly Ala Arg Ile Gly
 105

<210> 1112

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1112

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
 100 105

<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

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caagcgctac cagcggttgat gcgaggtttg agcgcctaac atg act gaa gat gac 115
 Met Thr Glu Asp Asp
 1 5

tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
 10 15 20

cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala
 25 30 35

gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
 40 45 50

cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
 55 60 65

tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
 70 75 80 85

atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
 90 95 100

gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
 105 110 115

gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
 120 125 130

ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu
 135 140 145

ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
 Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu
 150 155 160

tagcgctggg catgtgactt taa

615

<210> 1114

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1114

Met Thr Glu Asp Asp Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala
 1 5 10 15

Thr Gln Ala Leu Lys Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val
 20 25 30

Asp Pro Phe Gly Ala Val Val Phe Glu Asp His Asn Arg Asp Ala Asp
 35 40 45

Gly Asp Leu Thr Lys His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile
 50 55 60

Glu Asn Tyr Ser Ala Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser
 65 70 75 80

Thr Glu His Cys Ala Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu
 85 90 95

Gly Lys Ile Tyr Cys Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr
 100 105 110

Ala Lys Trp Gly Ala Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp
 115 120 125

Lys Ile Ser Pro Asn Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu
 130 135 140

Glu Val Leu Tyr Glu Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro
 145 150 155 160

Asn Lys Ala Leu

<210> 1115

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXA00717

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 Val Thr Pro Pro Ala
 1 5

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga 163
 Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly
 10 15 20

tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac 211
 Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn
 25 30 35

aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct 259
 Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala
 40 45 50

aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg 307
 Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met
 55 60 65

ggt ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg 355
 Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val
 70 75 80 85

ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att 403
 Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile
 90 95 100

gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc 451
 Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly
 105 110 115

gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc 499
 Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg
 120 125 130

atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt 547
 Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg
 135 140 145

ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt 595
 Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly
 150 155 160 165

gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc 643
 Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val
 170 175 180

ggt cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat 691
 Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp
 185 190 195

ggt gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag 739
 Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys
 200 205 210

act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc 787
 Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser
 215 220 225

gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac 835
 Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp
 230 235 240 245

ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc 883


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<210> 1116
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<212> PRT
<213> Corynebacterium glutamicum
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  1          5          10          15
Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly
          20          25          30
Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile
          35          40          45
Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp
  50          55          60

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Asp 65	Asp	Trp	Ser	Met	Gly 70	Phe	Leu	Asn	Arg	Asn 75	Asp	Ser	Asp	Gly	Val 80
Arg	Leu	Gln	Lys	Val 85	Leu	Ala	Gln	Ala	Gly 90	Val	Ala	Ser	Arg	Arg	His
Ala	Glu	Ile	Leu 100	Ile	Asp	Gln	Gly	Arg 105	Val	Glu	Val	Asn 110	Asp	Arg	Ile
Val	Thr	Thr 115	Gln	Gly	Val	Arg	Val 120	Asp	Pro	Asn	Asn 125	Asp	Val	Ile	Arg
Val 130	Asp	Gly	Val	Arg	Ile	His 135	Ile	Asn	Glu	Asp	Leu 140	Glu	Tyr	Phe	Val
Leu 145	Asn	Lys	Pro	Arg	Gly 150	Met	His	Ser	Thr	Met 155	Ser	Asp	Glu	Leu	Gly 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln
 165 170 175
 Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu
 180 185 190
 Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys
 195 200 205
 Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr
 210 215 220
 Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly
 225 230 235 240
 Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys
 245 250 255
 Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg
 260 265 270
 Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr
 275 280 285
 Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg
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 Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
 305 310 315 320

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 <211> 978
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(955)
 <223> RXA01894

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 acccatgaat gaaccggagc aacatcaccg gtccatgagg atg ccc aaa ccc aaa 115
 Met Pro Lys Pro Lys
 1 5
 aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly
 10 15 20
 ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp
 25 30 35
 tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

40	45	50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc			307
Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile			
55	60	65	
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg			355
Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met			
70	75	80	85
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc			403
Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe			
	90	95	100
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg			451
Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg			
	105	110	115
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga			499
Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly			
	120	125	130
agc ttc gct gcg atg ctg tgc ctg atg caa aac aat tcc atc ccg ggt			547
Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly			
	135	140	145
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tgc gat gtg			595
Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val			
150	155	160	165
ggc ggg tat atc gcg ggt gtg ttc ttt gga tgc cac cca atg gcg ccg			643
Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro			
	170	175	180
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc			691
Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val			
	185	190	195
tta gga tgc gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac			739
Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His			
	200	205	210
cac tgg tgg atg ggt gtg ata ttg ggt tgt gaa ata att atg tgc gcc			787
His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala			
	215	220	225
acg ttg ggt gac ttg gtt gag tgc cag ttc aaa cgc gat ttg ggc atc			835
Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile			
230	235	240	245
aag gat atg tgc aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt			883
Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg			
	250	255	260
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt			931
Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser			
	265	270	275
gtg atc agc agc tgc tat ccg tgc taaagcttgg gccagcttta agt			978
Val Ile Ser Ser Ser Tyr Pro Ser			
	280	285	

<210> 1118

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 1118

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 20 25 30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
 35 40 45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
 50 55 60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
 65 70 75 80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
 85 90 95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
 100 105 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
 115 120 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
 130 135 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
 145 150 155 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
 165 170 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
 180 185 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
 195 200 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
 210 215 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
 225 230 235 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
 245 250 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
 260 265 270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
 275 280 285

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<223> RXA02536
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185	190	195	
gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc			739
Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser			
200	205	210	
atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag			787
Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu			
215	220	225	
cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att			835
Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile			
230	235	240	245
cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act			879
Arg Glu Ala Leu Pro Val Leu			
250			

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<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 1120

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Gln	Gly	Ala	Arg	Val	Leu	Val	Phe	Pro	Glu	Ala	Thr	Ser	Gln	Ser	Phe
			20					25					30		

Gly	Thr	Gly	Arg	Leu	Asp	Thr	Gln	Ala	Glu	Glu	Leu	Asp	Gly	Glu	Phe
	35						40					45			

Ser	Thr	Ala	Val	Arg	Lys	Leu	Ala	Asp	Glu	Leu	Asp	Val	Val	Ile	Val
	50					55					60				

Ala	Gly	Met	Phe	Thr	Pro	Ala	Asp	Thr	Val	Gln	Arg	Gly	Glu	Lys	Thr
	65					70				75					80

Ile	Ser	Arg	Val	Asn	Asn	Thr	Val	Leu	Ile	Ser	Gly	Ala	Gly	Leu	His
				85					90					95	

Gln	Gly	Tyr	Asn	Lys	Ile	His	Thr	Tyr	Asp	Ala	Phe	Gly	Tyr	Arg	Glu
			100						105				110		

Ser	Asp	Thr	Val	Lys	Pro	Gly	Asp	Glu	Leu	Val	Val	Phe	Glu	Val	Asp
		115					120					125			

Asp	Ile	Lys	Phe	Gly	Val	Ala	Thr	Cys	Tyr	Asp	Ile	Arg	Phe	Pro	Glu
						135					140				

Gln	Phe	Lys	Asp	Leu	Ala	Arg	Asn	Gly	Ala	Gln	Ile	Ile	Val	Val	Pro
	145					150				155					160

Thr	Ser	Trp	Gln	Asp	Gly	Pro	Gly	Lys	Leu	Glu	Gln	Trp	Glu	Val	Leu
				165					170					175	

Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
 180 185 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
 195 200 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
 210 215 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
 225 230 235 240

Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
 245 250

<210> 1121
 <211> 1528
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1528)
 <223> RXN01209

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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

~~tcc ggc gga att tct atg atg cag ctg cgc gat aag aac tca ggc gtc 250~~

Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
 40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
 Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
 55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
 Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
 70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
 Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
 90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctc gat ccc gtc atg atc gcc acc
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
410 415 420

ggc gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
455 460 465

gcc gcc ggc gaa agc gtg gaa
1528

Ala Ala Gly Glu Ser Val Glu
470 475

<210> 1122

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

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20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

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370              375              380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
385              390              395              400
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
405              410              415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
420              425              430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
435              440              445
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
450              455              460
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
465              470              475

<210> 1123
<211> 1528
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1528)
<223> FRXA01209

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Met Cys Glu Arg Pro
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
90 95 100

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gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
455 460 465

gcc gcc ggc gaa agc gtg gaa
1528

Ala Ala Gly Glu Ser Val Glu
470 475

<210> 1124

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Lys Glu Leu Lys
 50 55 60
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

355	360	365
Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn		
370	375	380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met		
385	390	395 400
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr		
	405	410 415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn		
	420	425 430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg		
	435	440 445
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser		
	450	455 460
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu		
465	470	475

<210> 1125

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXN01617

<400> 1125

tcagaagcta cggcgggcgc cggcatccag gttgatttga agaccttcca gcatttaaga 60

tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca	115
Leu Ile Leu Lys Thr	
1 5	

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat	163
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asp	

10

15

20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc	211
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile	
25 30 35	

ggg atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg	259
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu	
40 45 50	

gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc	307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys	
55 60 65	

aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc	355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg	
70 75 80 85	

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu
 90 95 100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu
 105 110 115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val
 120 125 130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu
 135 140 145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp
 150 155 160 165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala
 170 175 180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys
 185 190 195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro
 200 205 210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt aaacaagctc 792
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 215 220

cct 795

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala
 1 5 10 15

Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu
 20 25 30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

<400> 1127																
gct	aat	cag	att	gag	gcc	gcc	acc	gca	gcg	cac	gat	ctt	gat	gtg	gtg	48
Ala	Asp	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val	
1			5			10			15							
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr	
			20			25			30							
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	
35			40			45										
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	
50			55			60										
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	
65		70		75		80										

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288
 Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95

gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336
 Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110

gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384
 Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125

gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140

ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160

acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

aaacaagctc cct 638

<210> 1128

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 1128

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
 50 55 60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
 65 70 75 80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

<210> 1129

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC01600

<400> 1129

tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttggagctg cgtgtccacc cttagatcta caatgtgata atg gtt tcg aag atg 115
 Met Val Ser Lys Met
 1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
 10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro
 25 30 35

ggt ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
 40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
 55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
 70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
 90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu
 105 110 115
 att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
 120 125 130
 cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
 135 140 145
 gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
 150 155 160 165
 gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
 170 175 180
 gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
 185 190 195
 gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
 200 205 210
 cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789
 His Gly Ile Val Pro Asp Met Lys Lys Leu
 215 220
 aaa 792

<210> 1130

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr
 1 5 10 15
 Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp
 20 25 30
 Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
 35 40 45
 His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
 50 55 60
 Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65 70 75 80
 Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
 85 90 95
 Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
 100 105 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
 210 215 220

<210> 1131

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXC01622

<400> 1131

aaggcgtggg cggtttttgaa ggagcttcgt ttggagcgcg gtcctttgga tcgtgaagtt 60

gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
 Met Ser Asp Phe Tyr
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
 90 95 100

gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
 105 110 115

cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
 120 125 130

ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
 135 140 145

aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
 150 155 160 165

tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met
 170 175 180

cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
 185 190 195

cct tca gat aat tagatgagtt ccgaaaattt aaa 726
 Pro Ser Asp Asn
 200

<210> 1132

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn
 1 5 10 15

Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
 20 25 30

Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
 35 40 45

Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
 50 55 60

Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
 65 70 75 80

Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
 85 90 95

Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
 100 105 110

Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
195 200

<210> 1133

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

ccatttttccg tttggtcttg cctaaagaac cgcattggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
Val Ser Lys Ile Ser
1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
25 30 35

~~taa ttt taa ggg taa caa aga aca caa gag ata gca ggg ccg acc ccg 255~~
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
 Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
 120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547
 Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
 135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
 Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
 150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643
 Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
 170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat 691
 Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
 185 190 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739
 Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
 200 205 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787
 Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp
 215 220 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg 835
 Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu
 230 235 240 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg 883
 Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg
 1027
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
 295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg
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 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
 310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg
 1123
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
 330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac
1171

Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg
1219

Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt
1267

Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga
1315

Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg
1363

Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act
1411

Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc
1459

Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
1507

Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
1555

Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
1603

Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
1651

Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
1699

Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
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1827

Val Ala Tyr

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<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 1134

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20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
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 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
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 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Ile
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

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Arg Ala Ala Pro Val Val Ala Tyr			
565			
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	Val Phe Glu Gln Ala		
	1 5		
ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg	163		
Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly			
	10 15 20		
ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc	211		
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser			
	25 30 35		
ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca	259		
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala			
	40 45 50		
cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc	307		
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr			
	55 60 65		
ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa	355		
Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys			
	70 75 80 85		
gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca	403		
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala			
	90 95 100		
atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa	451		
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu			
	105 110 115		
tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt	499		
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly			
	120 125 130		
atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc	552		
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser			
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gat

555

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<211> 144

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<213> Corynebacterium glutamicum

<400> 1136

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 20 25 30

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 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
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<210> 1137

<211> 898

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXC02207

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 Met Arg Arg Arg Ser
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cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
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ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg 211
 Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met
 25 30 35

ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc 259
 Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly
 40 45 50

caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt 307
 Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly
 55 60 65

gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc 355
 Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val
 70 75 80 85

tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa 403
 Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln
 90 95 100

tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc 451
 Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala
 105 110 115

gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg 499
 Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu
 120 125 130

cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat 547
 Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp
 135 140 145

cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc 595
 Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg
 150 155 160 165

gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag 643
 Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln
 170 175 180

ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc 691
 Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr
 185 190 195

tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt 739
 Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg
 200 205 210

gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt 787
 Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly
 215 220 225

ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att 835
 Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile
 230 235 240 245

gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc 883
 Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro
 250 255 260

cac cga cga gga acc
His Arg Arg Gly Thr
265

898

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<213> Corynebacterium glutamicum

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20 25 30
Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
35 40 45
Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
50 55 60
Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
65 70 75 80
Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
85 90 95
Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
100 105 110
Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
115 120 125
Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
130 135 140
Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145 150 155 160
Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
165 170 175
Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
180 185 190
Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
195 200 205
Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
210 215 220
Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225 230 235 240
Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu
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Gln Asn Asp Arg Pro His Arg Arg Gly Thr
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Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr				
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acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta				739
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu				
	200	205	210	
acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac				787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp				
	215	220	225	
gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc				835
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg				
	230	235	240	245
atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaacgcacg				888
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<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 1140

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35 40 45

Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu
50 55 60

Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val
65 70 75 80

Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro
85 90 95

Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile
100 105 110

Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg
115 120 125

Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile
130 135 140

Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn
145 150 155 160

Gly Lys Ser Ile Ile Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr
 165 170 175

Trp Leu Lys Glu Tyr Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe
 180 185 190

Leu Gly Asp Asp Thr Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn
 195 200 205

Asp Asp Arg Ala Leu Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala
 210 215 220

Lys Thr Arg Val Asp Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys
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 Met Ala Arg Pro Ile
 1 5

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 Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala
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ggg cgt tca ttt ggt ttt gcg cag gcc aaa gcc cag ctt ccc tat ctg 211
 Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu
 25 30 35

aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259
 Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala
 40 45 50

atg cca gat tcc aat cat ggc tac gat gtc att gat ccc acc acc atc 307
 Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
 55 60 65

aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355
 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala
 70 75 80 85

aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403
 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His

90	95	100	
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Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu	110	115	
105			
aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg			499
Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp	125	130	
120			
cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt			547
His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly Met Pro Ile Leu Gly	140	145	
135			
gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag			595
Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu	155	160	
150		165	
aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc			643
Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr	175	180	
170			
gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg			691
Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu	190	195	
185			
cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg			739
Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val	205	210	
200			
aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat			787
Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His	220	225	
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act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc			835
Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly	235	240	
230		245	
gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg			883
Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu	255	260	
250			
cac aga ctc cgc gac ctc att gga cct gag cgc tgg ctg atc atc gaa			931
His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu	270	275	
265			
aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat			979
Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp	285	290	
280			
ggc acc act ggc tac gac gcc ctc cgt gaa ctc gac ggc gtg ttt atc			
1027			
Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile	300	305	
295			
tcc cga gaa tct gag gac aaa ttc tcc atg ctg gcg ctg acc cac agt			
1075			
Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser	315	320	
310		325	

gga tcc acc tgg gat gaa cgc gcc ctc aaa tcc acg gag gaa agc ctc
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 Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu
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 1171
 Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu
 345 350 355

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 Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val
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acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg
 1267
 Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met
 375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc
 1315
 Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr
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 Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
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 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly
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 Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr
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 1651
 His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
 505 510 515

tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg
1699

Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala
520 525 530

gtg ctc ccc gcg cca gac ggc gca acg ggc agt ttc ctc cta caa aac
1747

Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn
535 540 545

ctg ctg ggc gta tgg ccc gcc gac ggc gtg atc acc gat gcg ctg cgc
1795

Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg
550 555 560 565

gat cga ttc agg gaa tac gcc cta aaa gct atc cgc gaa gca tcc aca
1843

Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
570 575 580

aaa acc acg tgg gtg gac ccc aac gag tcc ttc gag gct gcg gtc tgc
1891

Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
585 590 595

gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc
1939

Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr
600 605 610

gaa ttt gtc tcc cac atc aac cgt ggc tct gtg caa atc tcc tta ggc
1987

Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly
615 620 625

agg aaa ctg ctg caa atg gtg ggc gct gga atc ccc gac act tac caa
2035

Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln
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gga act gag ttt tta gaa gac tcc ctg gta gat ccc gat aac cga cgc
2083

~~Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg~~
650 655 660

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2131

Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr
665 670 675

tgg gct tgg acg cag gtt aat tcg gta gaa gac ttg gtg gat aac gcc
2179

Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala
680 685 690

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Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
695 700 705

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Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly
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730 735 740

cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc
2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
745 750 755

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2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly
760 765 770

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2467

Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val
775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta
2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu
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2556

Val Pro Asp Ser Glu Phe
810

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Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser
35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
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Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
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Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
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Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Phe	Asp	Ile	Asp	Trp	His	Glu	Asp	Asn	Gly	Ser	Gly	Gly	Lys	Leu	Gly	
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Met	Pro	Ile	Leu	Gly	Ala	Glu	Gly	Asp	Glu	Asp	Lys	Leu	Glu	Phe	Ala	
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Glu	Leu	Asp	Gly	Glu	Lys	Val	Leu	Lys	Tyr	Phe	Asp	His	Leu	Phe	Pro	
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Gln	His	Tyr	Arg	Leu	Gln	Phe	Trp	Arg	Asp	Gly	Val	Ile	Asn	Phe	Arg	
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Trp	Leu	Ile	Ile	Glu	Lys	Ile	Leu	Ser	Val	Asp	Glu	Pro	Leu	Asp	Pro	
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Ala	Gly	Thr	Asn	Val	Thr	Glu	Asp	Lys	Leu	Ser	Glu	Thr	Ile	Ile	Glu	
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Arg	Arg	Asp	Ala	Leu	Asp	Leu	Ile	Ala	Ala	Ala	Leu	Leu	Gly	Asn	Gly	
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 Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
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 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
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 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
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 530 535 540
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 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
 595 600 605
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
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 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
 625 630 635 640
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp
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 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
 660 665 670
 Glu Arg Leu Gln Thr Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp
 675 680 685
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser
 690 695 700
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
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 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
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Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr
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Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
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<211> 2556

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<213> Corynebacterium glutamicum

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atg cca gat tcc aat cat ggc tac gat ctc att gat ccc acc acc atc 307

Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
 55 60 65

aat gaa gag ctc ggt ggc atg gag ggt ctt cga gat ctt gcc gca gct 355
 Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala
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 Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His
 90 95 100

tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta 451
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 Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr
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 185 190 195

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 Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His
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 Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu
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 Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp
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1267

Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met
375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc
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Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr
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Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
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gac ctc atc gcg gcc gcc cta ctt ggc aat ggc gag gcc aaa atc cgc
1411

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425 430 435

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440 445 450

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1555

Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln
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1603

Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr
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1651

His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
505 510 515

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1699

Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala
520 525 530

gtg ctc ccc gcg cca gac ggc gca acg ggc agt ttc ctc cta caa aac
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Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn
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Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg
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1843

Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
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aaa acc acg tgg gtg gac ccc aac gag tcc ttc gag gct gcg gtc tgc
1891

Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
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gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc
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Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr
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Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly
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Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala
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gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct
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Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
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Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
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Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly
760 765 770

gga caa tgg gaa gac agg ctc acc ggg caa cgc ttc agt ggt gtt gtc
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Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val
775 780 785

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Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu
790 795 800 805

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Val Pro Asp Ser Glu Phe
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His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met
                25                30                35

ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta 259
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val
                40                45                50

cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc 307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly
                55                60                65

agc tgg tgg cgc gcc gag atc gcg ccc aag gcc ggc gat cgt tac ggt 355
Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly
                70                75                80                85

ttt tcg ctt ttc gac ggc tcc tcc tgg tca aaa acc ctc ccc gat ccc 403
Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro
                90                95                100

cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc 451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser
                105                110                115

gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc 499
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu
                120                125                130

cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat 547
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp
                135                140                145

gga acg ttt gag gga gtc gtc gac aag ctt cct tat ctg cgc gac ctc 595
Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu
                150                155                160                165

ggc gtg acc gcc atc gaa ctt tta ccc gtg cag ccc ttt ggc ggc aac 643

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Gly Val Thr Ala	Ile Glu Leu Leu Pro Val Gln Pro Phe Gly Gly Asn	
	170	175 180
cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc		691
Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly	185	190 195
tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag		739
Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln	200	205 210
gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc		787
Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro	215	220 225
gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc		835
Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser	230	235 240 245
acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa		883
Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu	250	255 260
gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt		931
Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe	265	270 275
cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc		979
His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg	280	285 290
ggc gcc tat tcc cta ctt gcg cag ctg acc atg gtg gcc gag gat gtc		
1027		
Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val	295	300 305
tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc		
1075		
Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu	310	315 320 325
aat gac ccc aag ttc gtt acc tcc cgc gag gcc ggc ggt ttt ggc ctg		
1123		
Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu	330	335 340
gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt		
1171		
Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val	345	350 355
tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca		
1219		
Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr	360	365 370
tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc		
1267		
Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser	375	380 385

gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca
1891

Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr
585 590 595

acc ctt cag ccg tgg ggc ttt gcg atc ctg acc cga aac tagaaaaagg
1940

Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr Arg Asn
600 605 610

ccacctcgat tga
1953

<210> 1146

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 1146

Met Leu Lys Asp Leu Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met
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Cys His Ser Ile Ser His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr
20 25 30

Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro
35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met
50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc
1315

Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr
390 395 400 405

cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc
1363

Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly
410 415 420

aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag
1411

Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln
425 430 435

cag gtg ttg aag gca gcc att atc tac agc tcg ccg tat acc ccg atg
1459

Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met
440 445 450

ttg ttt atg ggt gaa gaa ttc gga gcc acc acc cca ttc gcc ttc ttt
1507

Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr Pro Phe Ala Phe Phe
455 460 465

tgc tcc cac acc gac ccc gag ctc aac cgg cta acc tcc gag ggc cgc
1555

Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg
470 475 480 485

aaa cgg gaa ttc gca cgc ctt ggc tgg aac gcc gac gac atc ccc tcc
1603

Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser
490 495 500

ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc
1651

Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe
505 510 515

act gcg gag cag cgc cgc atc aac gac gct tac aag cag ctg ttg cac
1699

Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr Lys Gln Leu Leu His
520 525 530

ctg cgg cac acc ttg ggc ttc tcc caa cca aac ttg ctc aca ctc gag
1747

Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn Leu Leu Thr Leu Glu
535 540 545

gtt gag cac ggc gag aac tgg cta tcg atg gcc aat ggt cgc ggc cga
1795

Val Glu His Gly Glu Asn Trp Leu Ser Met Ala Asn Gly Arg Gly Arg
550 555 560 565

att ctg gcg aat ttc tcc gac gac acc atc acc gtc ccg ctt ggc ggc
1843

Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly
570 575 580

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr
 225 230 235 240
 Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly
 245 250 255
 His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln
 260 265 270
 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His
 275 280 285
 Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met
 290 295 300
 Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile
 305 310 315 320
 Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala
 325 330 335
 Gly Gly Phe Gly Leu Asp Ala Gln Trp Val Asp Asp Ile His His Ala
 340 345 350
 Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe
 355 360 365
 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His
 370 375 380
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val
 385 390 395 400
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr
 405 410 415
 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr
 420 425 430
 Leu Thr Pro Glu Gln Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser
 435 440 445
 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr
 450 455 460
 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu
 465 470 475 480
 Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala
 485 490 495
 Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys
 500 505 510
 Leu Asp Trp Glu Phe Thr Ala Glu Gln Arg Arg Ile Asn Asp Ala Tyr
 515 520 525
 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn
 530 535 540

Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala
545 550 555 560

Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr
565 570 575

Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val
580 585 590

Thr Asp Thr Ser Thr Thr Leu Gln Pro Trp Gly Phe Ala Ile Leu Thr
595 600 605

Arg Asn
610

<210> 1147

<211> 832

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(832)

<223> RXN02355

<400> 1147

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tagattgata agcatctgtt gttaagaaag gtgacttcct atg tcc tcg att tcc 115
Met Ser Ser Ile Ser
1 5

cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163
Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile
10 15 20

gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211
Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser
25 30 35

acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259
~~Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met~~
40 45 50

ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307
Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn
55 60 65

gaa gcc cac ccc gat gag cag gta acg ctc aac gaa ctc gcc ggt gaa 355
Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu
70 75 80 85

gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403
Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn
90 95 100

tct gac tac gac gtc atg gcg ctc gac gtc atc tgg acc gca gaa ttc 451
Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe
105 110 115

gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp
 120 125 130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly
 135 140 145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg
 150 155 160 165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val
 170 175 180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr
 185 190 195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile
 200 205 210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg
 215 220 225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly
 230 235 240

<210> 1148

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 1148

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Leu Leu Ala Ala Ile Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser
 20 25 30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro
 35 40 45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile
 50 55 60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn
 65 70 75 80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser
 85 90 95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile
 100 105 110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser		
130	135	140
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly		
145	150	155
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn		
165	170	175
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val		
180	185	190
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn		
195	200	205
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp		
210	215	220
Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala		
225	230	235
		240
Leu Val Asp Gly		

<210> 1149
 <211> 609
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(586)
 <223> RXN02909

<400> 1149
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 atagtttccct ggattgtttg gcacagtcgg gagaaaactc atg aac cgc gca cga 115
 Met Asn Arg Ala Arg

atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt	163
Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys	
10	15
20	
ggg tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat	211
Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn	
25	30
35	
att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att	259
Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile	
40	45
50	
tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act	307
Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr	
55	60
65	
ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag	355

Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu
 70 75 80 85

caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp
 90 95 100

ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His
 105 110 115

aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr
 120 125 130

tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg
 135 140 145

cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taaggtgcca 596
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser
 150 155 160

gggctttaaa gtg 609

<210> 1150

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 1150

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 20 25 30

Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile
 35 40 45

Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser
 50 55 60

Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe
 65 70 75 80

Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr
 85 90 95

Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln
 100 105 110

Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe
 115 120 125

Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val
 130 135 140

Asp Glu Leu Asp Arg Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro
 145 150 155 160

Thr Ser

<210> 1151
 <211> 1590
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1567)
 <223> RXS00349

<400> 1151
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 Met Leu Ser Phe Ala
 1 5
 acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct 163
 Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro
 10 15 20
 ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg 211
 Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val
 25 30 35
 gcc ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct 259
 Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser
 40 45 50
 tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc 307
 Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr
 55 60 65
 tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg 355
 Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr
 70 75 80 85
 atg acc atg ttc acc aac atg ggt gta gag agg aag atg ccg gtc aac 403
 Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn
 90 95 100
 gtg ttt cat gtt gta ggc aag ttg gac acc aac ttc tcc aaa ctg tct 451
 Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser
 105 110 115
 gag gtt gac cgt ttg atc cgt tcc att cag gct ggt gcg acc ccg cct 499
 Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro
 120 125 130
 gag gtt gcc gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct 547
 Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser
 135 140 145
 tat ggt ttc cct gtt gcg ttg ctt ggc tgg gca atg atg ggt ggt gct 595
 Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala
 150 155 160 165

gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt 643
 Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe
 170 175 180

att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag 691
 Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys
 185 190 195

ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg 739
 Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr
 200 205 210

ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag 787
 Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu
 215 220 225

atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca 835
 Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala
 230 235 240 245

ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg 883
 Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro
 250 255 260

gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc 931
 Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly
 265 270 275

att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat 979
 Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His
 280 285 290

gtc atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct
 1027
 Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser
 295 300 305

aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca
 1075
 Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala
 310 315 320 325

gtg ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act
 1123
 Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr
 330 335 340

gcg ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc
 1171
 Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly
 345 350 355

ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt
 1219
 Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly
 360 365 370

ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att
 1267
 Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile

375 380 385
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg
 1315
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met
 390 395 400 405
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg
 1363
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala
 410 415 420
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt
 1411
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly
 425 430 435
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac
 1459
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr
 440 445 450
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag
 1507
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu
 455 460 465
 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc
 1555
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe
 470 475 480 485
 ggt aat aaa agg taaaaatcaa cctgcttagg cgt
 1590
 Gly Asn Lys Arg

<210> 1152

<211> 489

<212> PRT

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<400> 1152

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 cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163
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Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp
355 360

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				199 33 005.0	14 July 1999 (14.07.1999)	DE
				199 33 006.9	14 July 1999 (14.07.1999)	DE
				60/148.613	12 August 1999 (12.08.1999)	US
(21) International Application Number: PCT/IB00/00923				199 40 764.9	27 August 1999 (27.08.1999)	DE
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(22) International Filing Date: 23 June 2000 (23.06.2000)				199 40 766.5	27 August 1999 (27.08.1999)	DE
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199 30 476.9	1 July 1999 (01.07.1999)	DE		199 42 129.3	3 September 1999 (03.09.1999)	DE
60/142.101	2 July 1999 (02.07.1999)	US		199 42 076.9	3 September 1999 (03.09.1999)	DE
199 31 415.2	8 July 1999 (08.07.1999)	DE		199 42 079.3	3 September 1999 (03.09.1999)	DE
199 31 418.7	8 July 1999 (08.07.1999)	DE		199 42 086.6	3 September 1999 (03.09.1999)	DE
199 31 419.5	8 July 1999 (08.07.1999)	DE		199 42 087.4	3 September 1999 (03.09.1999)	DE
199 31 420.9	8 July 1999 (08.07.1999)	DE		199 42 088.2	3 September 1999 (03.09.1999)	DE
199 31 424.1	8 July 1999 (08.07.1999)	DE		199 42 095.5	3 September 1999 (03.09.1999)	DE
199 31 428.4	8 July 1999 (08.07.1999)	DE		199 42 124.2	3 September 1999 (03.09.1999)	DE
199 31 434.9	8 July 1999 (08.07.1999)	DE		60/187,970	9 March 2000 (09.03.2000)	US
199 31 435.7	8 July 1999 (08.07.1999)	DE				
199 31 443.8	8 July 1999 (08.07.1999)	DE				
199 31 453.5	8 July 1999 (08.07.1999)	DE	(71) Applicant: BASF AKTIENGESELLSCHAFT [DE/DE]; D-67056 Ludwigshafen (DE).			
199 31 457.8	8 July 1999 (08.07.1999)	DE				
199 31 465.9	8 July 1999 (08.07.1999)	DE	(72) Inventors: POMPEJUS, Markus; Wenjenstr. 21, D-67251 Freinsheim (DE). KRÖGER, Burkhard; Im Waldhof 1, D-67117 Limburgerhof (DE). SCHRÖDER, Hartwig; Goethestr. 5, D-69226 Nussloch (DE). ZELDER, Oskar; Rossmarktstr. 27, D-67346 Speyer (DE). HABERHAUER, Gregor; Moselstr. 42, D-67117 Limburgerhof (DE).			
199 31 478.0	8 July 1999 (08.07.1999)	DE				
199 31 510.8	8 July 1999 (08.07.1999)	DE				
199 31 541.8	8 July 1999 (08.07.1999)	DE				
199 31 573.6	8 July 1999 (08.07.1999)	DE				
199 31 592.2	8 July 1999 (08.07.1999)	DE				
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199 32 126.4	9 July 1999 (09.07.1999)	DE				
199 32 130.2	9 July 1999 (09.07.1999)	DE				
199 32 186.8	9 July 1999 (09.07.1999)	DE				
199 32 206.6	9 July 1999 (09.07.1999)	DE				
199 32 227.9	9 July 1999 (09.07.1999)	DE				
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199 32 922.2	14 July 1999 (14.07.1999)	DE				
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199 32 928.1	14 July 1999 (14.07.1999)	DE				

[Continued on next page]

(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

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IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(88) Date of publication of the international search report:
29 March 2001

Published:

— With international search report.

— Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00923

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/61 C12N1/21 C12N9/90 C07K14/34
C12P13/08 C12Q1/68
/(C12N15/61,C12R1:15)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12P C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, EMBL, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KEILHAUER C ET AL: "ISOLEUCINE SYNTHESIS IN CORYNEBACTERIUM GLUTAMICUM: MOLECULAR ANALYSIS OF THE ILVB-ILVN-ILVC OPERON" JOURNAL OF BACTERIOLOGY,US,WASHINGTON, DC, vol. 175, no. 17, 1 September 1993 (1993-09-01), pages 5595-5603, XP000611312 ISSN: 0021-9193 the whole document ---	1-3, 8-19, 22-34
	-/--	

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *&* document member of the same patent family

Date of the actual completion of the international search

31 October 2000

Date of mailing of the international search report

24. 01. 01

Name and mailing address of the ISA

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NL - 2280 HV Rijswijk
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Fax: (+31-70) 340-3016

Authorized officer

Galli, I

INTERNATIONAL SEARCH REPORT

International Application No

PC., IB 00/00923

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category - Citation of document, with indication, where appropriate, of the relevant passages

Relevant to claim No.

- X DATABASE EMBL SEQUENCES [Online]
Accession No. 033231,
15 December 1998 (1998-12-15)
COLE S.T.: "Diaminopimelate epimerase
(DAPf) of Mycobacterium tuberculosis."
XP002151647
52% identity at amino acid level with Seq.
ID 2.
-& COLE S.T. ET AL.: "Deciphering the
biology of Mycobacterium tuberculosis from
the complete genome sequence."
NATURE,
vol. 393, 1998, pages 537-544, XP002151645

- A BATHE B. ET AL.: "A physical and genetic
map of the Corynebacterium glutamicum
ATCC13032 chromosome."
MOL. GEN. GENET.,
vol. 252, 1996, pages 255-265, XP002151646
the whole document, in particular table 3.

- A EP 0 435 132 A (KERNFORSCHUNGSANLAGE
JUELICH) 3 July 1991 (1991-07-03)
the whole document

- A EIKMANNS B J ET AL: "MOLECULAR ASPECTS OF
LYSINE, THREONINE, AND ISOLEUCINE
BIOSYNTHESIS IN CORYNEBACTERIUM
GLUTAMICUM"
ANTONIE VAN LEEUWENHOEK, DORDRECHT, NL,
vol. 64, no. 2, 1993, pages 145-163,
XP000918559
figure 1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 00/00923

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-38 Partially.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-38, partly

An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein or a portion thereof, said nucleic acid being characterized by sequence ID 1. An isolated nucleic acid comprising a nucleotide sequence at least 50% homologous to seq. 1. Corresponding polypeptides (Seq. ID 2). Corresponding vectors, recombinant host cells, production methods. Use in diagnosis of *C. diphtheriae*.

